

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: STUYVER, LIEVEN  
ROSSAU, RUDI  
MAERTENS, GEERT

(ii) TITLE OF INVENTION: METHOD FOR TYPING AND DETECTING HBV

(iii) NUMBER OF SEQUENCES: 313

(iv) CORRESPONDENCE ADDRESS:

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(D) STATE: VIRGINIA  
(E) COUNTRY: U.S.A.  
(F) ZIP: 22201-4714

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US 09/155,885  
(B) FILING DATE: 08-OCT-1998  
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

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(B) FILING DATE: 21-APR-1997  
(C) CLASSIFICATION:

(viii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 96870053.4  
(B) FILING DATE: 19-APR-1996  
(C) CLASSIFICATION:

(ix) ATTORNEY/AGENT INFORMATION:

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(B) REGISTRATION NUMBER: 36,663  
(C) REFERENCE/DOCKET NUMBER: 2551-5

(x) TELECOMMUNICATION INFORMATION:

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(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

GGGTCAACCATTCTTGGG

19

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

GAACAAGAGCTACAGCATGG G

21

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

CCACTGCATGGCCTGAGGAT G

21

(2) INFORMATION FOR SEQ ID NO: 4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

GTTCCKGAAAC TGGAGGCCACC AG

22

(2) INFORMATION FOR SEQ ID NO: 5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

TCTTTGTATT AGGAGGGCTGT AG

22

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCTGTAGGCA TAAATTGGTC TG

22

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CTCCACAGWA GCTCCAAATT C

21

(2) INFORMATION FOR SEQ ID NO: 8:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

GAAGGAAAGA AGTCAGAAGG C

21

(2) INFORMATION FOR SEQ ID NO: 9:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

TGGCTTTGGG GCATGG

16

(2) INFORMATION FOR SEQ ID NO: 10:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

TGGCTTTAGG GCATGG

16

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

TGGCTTTAGG ACATGG

16

(2) INFORMATION FOR SEQ ID NO: 12:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

AAGTTGCATG GTGCTG

16

(2) INFORMATION FOR SEQ ID NO: 13:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

CACCTCTGCC TAATCAT

17

(2) INFORMATION FOR SEQ ID NO: 14:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

TGGGGTGGAG CCCTCAG

17

(2) INFORMATION FOR SEQ ID NO: 15:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

GCCAGCAGCC AACCAAG

16

(2) INFORMATION FOR SEQ ID NO: 16:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

CCCATGGGGG ACTGT

15

(2) INFORMATION FOR SEQ ID NO: 17:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

AACCCCAACA AGGATG

16

(2) INFORMATION FOR SEQ ID NO: 18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

TCCACCAGCA ATCCT

15

(2) INFORMATION FOR SEQ ID NO: 19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

TGGGGGAAGA ATATTT

16

(2) INFORMATION FOR SEQ ID NO: 20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

AAATTCCAGC AGTCCC

16

(2) INFORMATION FOR SEQ ID NO: 21:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GTTCCCAACC CTCTGG

16

(2) INFORMATION FOR SEQ ID NO: 22:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

AACCTCGCAA AGGCAT

16

(2) INFORMATION FOR SEQ ID NO: 23:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

TGCATTCAAA GCCAAC

16

(2) INFORMATION FOR SEQ ID NO: 24:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

TACTCACAAAC TGTGCC

16

(2) INFORMATION FOR SEQ ID NO: 25:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

ACCCTGCGTT CGGAGC

16

(2) INFORMATION FOR SEQ ID NO: 26:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

CAGGAAGACA GCCTAC

16

(2) INFORMATION FOR SEQ ID NO: 27:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

GATCCAGCCT TCAGAG

16

(2) INFORMATION FOR SEQ ID NO: 28:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

ATGCTCCAGC TCCTAC

16

(2) INFORMATION FOR SEQ ID NO: 29:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

GCTTCCTTGG ACGGTC

16

(2) INFORMATION FOR SEQ ID NO: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

CTACCCCAAT CACTCC

16

(2) INFORMATION FOR SEQ ID NO: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

AGCACCTCTC TCAACG

16

(2) INFORMATION FOR SEQ ID NO: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

CCAATGGCAA ACAAGG

16

(2) INFORMATION FOR SEQ ID NO: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

CTGAGGGCTC CACCCA

17

(2) INFORMATION FOR SEQ ID NO: 34:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

ATCTCTTGTA CATGTC

16

(2) INFORMATION FOR SEQ ID NO: 35:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

ATCTCTTGTA CATGTC

16

(2) INFORMATION FOR SEQ ID NO: 36:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

ATCTCATGTT CATGTC

16

(2) INFORMATION FOR SEQ ID NO: 37:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

CAGTGGGACA TGTACA

16

(2) INFORMATION FOR SEQ ID NO: 38:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

CAGTAGGACA TGAACA

16

(2) INFORMATION FOR SEQ ID NO: 39:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

CTGTTCAAGC CTCCAA

16

(2) INFORMATION FOR SEQ ID NO: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

AGCCTCCAAG CTGTGC

16

(2) INFORMATION FOR SEQ ID NO: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

AAAGCCACCC AAGGCA

16

(2) INFORMATION FOR SEQ ID NO: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

TGGCTTTAGG ACATGGA

17

(2) INFORMATION FOR SEQ ID NO: 43:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

GACATGTACA AGAGATGA

18

(2) INFORMATION FOR SEQ ID NO: 44:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

GACATGAACA TGAGATGA

18

(2) INFORMATION FOR SEQ ID NO: 45:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

TGTACATGTC CCACTGTT

18

(2) INFORMATION FOR SEQ ID NO: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

TGTTCATGTC CTACTGTT

18

(2) INFORMATION FOR SEQ ID NO: 47:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

ACTGTTCAAG CCTCCAAG

18

(2) INFORMATION FOR SEQ ID NO: 48:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

GGCACAGGCT TGGAGGCTT

19

(2) INFORMATION FOR SEQ ID NO: 49:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

AAAGCCACCC AAGGCACA

18

(2) INFORMATION FOR SEQ ID NO: 50:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

CCCAAGAGGGT TGGGAAC

17

(2) INFORMATION FOR SEQ ID NO: 51:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

CAGCATGGGG CAGAATCT

18

(2) INFORMATION FOR SEQ ID NO: 52:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

TCCACCAGCA ATCCTCTG

18

(2) INFORMATION FOR SEQ ID NO: 53:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

GGATCCAGCC TTCAGAGC

18

(2) INFORMATION FOR SEQ ID NO: 54:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TCAGGAAGAC AGCCTAC

17

(2) INFORMATION FOR SEQ ID NO: 55:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

TTCAACCCCA ACAAGGATC

19

(2) INFORMATION FOR SEQ ID NO: 56:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

AATGCTCCAG CTCCTAC

17

(2) INFORMATION FOR SEQ ID NO: 57:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

CTGCATTCAA AGCCAATC

18

(2) INFORMATION FOR SEQ ID NO: 58:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCCCATGGGG GACTGTTG

18

(2) INFORMATION FOR SEQ ID NO: 59:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

CATACTCACA ACTGTGCCA

19

(2) INFORMATION FOR SEQ ID NO: 60:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GGGCTTTCTT GGACGGTCC

19

(2) INFORMATION FOR SEQ ID NO: 61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CTCTCGAATG GGGGAAGA

18

(2) INFORMATION FOR SEQ ID NO: 62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

CCTACCCCCAA TCACTCCA

18

(2) INFORMATION FOR SEQ ID NO: 63:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

AGCACCTCTC TCAACGACA

19

(2) INFORMATION FOR SEQ ID NO: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCAAATTCCA GCAGTCCCG

19

(2) INFORMATION FOR SEQ ID NO: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

GCCAATGGCA AACAAAGGTA

19

(2) INFORMATION FOR SEQ ID NO: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

GACATGAACA TGAGATG

17

(2) INFORMATION FOR SEQ ID NO: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

GGACATGAAC AAGAGAT

17

(2) INFORMATION FOR SEQ ID NO: 68:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

GACATGTACA AGAGATG

17

(2) INFORMATION FOR SEQ ID NO: 69:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

ACATAAGAGG ACTCTTGGAC

20

(2) INFORMATION FOR SEQ ID NO: 70:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

TACTTCAAAG ACTGTGTGTT TA

22

(2) INFORMATION FOR SEQ ID NO: 71:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

ACAAAGACCT TTAAYCT

17

(2) INFORMATION FOR SEQ ID NO: 72:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

ACAAAGATCA TTAAYCT

17

(2) INFORMATION FOR SEQ ID NO: 73:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

TTCCACCAGC AATCCTC

17

(2) INFORMATION FOR SEQ ID NO: 74:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

GATCCAGCCT TCAGAGC

17

(2) INFORMATION FOR SEQ ID NO: 75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

CAAGGTATGT TGCCCGTTG TCC

23

(2) INFORMATION FOR SEQ ID NO: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

CCAAACAGTG GGGGAAAGCC C

21

(2) INFORMATION FOR SEQ ID NO: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

CTACGGATGG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

TACGGACGGA AACTGC

16

(2) INFORMATION FOR SEQ ID NO: 79:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

TTCGGACGGA AACTGC

16

(2) INFORMATION FOR SEQ ID NO: 80:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

CTTCGGACGG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 81:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

CTACGGATAG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 82:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CTTCGGACAG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 83:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

CTATGGGAGT GGGCCTCAGY C

21

(2) INFORMATION FOR SEQ ID NO: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

GCTGTAGGCA TAAATTGGTC TG

22

(2) INFORMATION FOR SEQ ID NO: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

CTCCACAGWA GCTCCAAATT C

21

(2) INFORMATION FOR SEQ ID NO: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

ACATAAGAGG ACTCTTGGAC

20

(2) INFORMATION FOR SEQ ID NO: 87:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

TACTTCAAAG ACTGTGTGTT TA

22

(2) INFORMATION FOR SEQ ID NO: 88:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

TAGGTTAAAG GTCTTTGT

18

(2) INFORMATION FOR SEQ ID NO: 89:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TAGGTTAACG ATCTTTGT

18

(2) INFORMATION FOR SEQ ID NO: 90:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CATGCCCCAC TGTTCAA

17

(2) INFORMATION FOR SEQ ID NO: 91:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

CATGTCCTAC TGTTCAA

17

(2) INFORMATION FOR SEQ ID NO: 92:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

TTCTGCCCCA TGCTGTA

17

(2) INFORMATION FOR SEQ ID NO: 93:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

TTCTGCCCCA TGCTGTAG

18

(2) INFORMATION FOR SEQ ID NO: 94:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 21 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

GGTAWAAAGG GACTCAMGAT G

21

(2) INFORMATION FOR SEQ ID NO: 95:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

TCAGCTATAT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 96:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CAGCTATATG GATGAT

16

(2) INFORMATION FOR SEQ ID NO: 97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

TTCAGCTATA TGGATG

16

(2) INFORMATION FOR SEQ ID NO: 98:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

TCAGTTATAT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 99:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

TTTCAGTTAT ATGGATG

17

(2) INFORMATION FOR SEQ ID NO: 100:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

TTTAGTTATA TGGATGA

17

(2) INFORMATION FOR SEQ ID NO: 101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

TCAGCTATGT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

TCAGTTATGT GGATGAT

17

(2) INFORMATION FOR SEQ ID NO: 103:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

TTTCAGCTAT GTGGATG

17

(2) INFORMATION FOR SEQ ID NO: 104:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 23 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CAAGGTATGT TGCCCGTTTG TCC

23

(2) INFORMATION FOR SEQ ID NO: 105:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

GGYAWAAAGG GACTCAMGAT G

21

(2) INFORMATION FOR SEQ ID NO: 106:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GGGTCACCAT ATTCTTGGG

19

(2) INFORMATION FOR SEQ ID NO: 107:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 22 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GTTCCKGAAAC TGGAGCCACC AG

22

(2) INFORMATION FOR SEQ ID NO: 108:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 40 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

CCGGAAAGCT TGAGCTCTTC TTTTCACCT CTGCCTAAC

40

(2) INFORMATION FOR SEQ ID NO: 109:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 40 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CCGGAAAGCT TGAGCTCTTC AAAAAGTTGC ATGGTGCTGG

40

(2) INFORMATION FOR SEQ ID NO: 110:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

GTGGTTCGCC GGGCTTG

17

(2) INFORMATION FOR SEQ ID NO: 111:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 25 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CTGCGAGGCG AGGGAGTTCT TCTTC

25

(2) INFORMATION FOR SEQ ID NO: 112:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 27 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

TGCCATTGT TCAGTGGTTC GTAGGGC

27

(2) INFORMATION FOR SEQ ID NO: 113:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 25 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

CCGGCAGATG AGAAGGCACA GACGG

25

(2) INFORMATION FOR SEQ ID NO: 114:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

TTCAGCTATA TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 115:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

TCAGCTATAT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 116:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

TTCAGCTATG TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 117:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

TCAGCTATGT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

GGCTTTGGGG CATGG

15

(2) INFORMATION FOR SEQ ID NO: 119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

TGGCTTTGGG GCATG

15

(2) INFORMATION FOR SEQ ID NO: 120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

GTGGCTTTGG GGCATG

16

(2) INFORMATION FOR SEQ ID NO: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

GGCTTTGGGG CATGGA

16

(2) INFORMATION FOR SEQ ID NO: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

TGGCTTTGGG ACATGG

16

(2) INFORMATION FOR SEQ ID NO: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

GGCTTTGGGA CATGG

15

(2) INFORMATION FOR SEQ ID NO: 124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

TGGCTTTGGG ACATG

15

(2) INFORMATION FOR SEQ ID NO: 125:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

GTGGCTTTGG GACATG

16

(2) INFORMATION FOR SEQ ID NO: 126:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

GGCTTTGGGA CATGGA

16

(2) INFORMATION FOR SEQ ID NO: 127:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

TCAGTTATAT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 128:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

TTCAGTTATA TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 129:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

TTTCAGTTAT ATGGATGAT

19

(2) INFORMATION FOR SEQ ID NO: 130:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

TCAGTTATGT GGATGATG

18

(2) INFORMATION FOR SEQ ID NO: 131:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

TTCACTTATG TGGATGAT

18

(2) INFORMATION FOR SEQ ID NO: 132:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

TTTCAGTTAT GTGGATGAT

19

(2) INFORMATION FOR SEQ ID NO: 133:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

TTTCAGTTAT GTGGATGA

18

(2) INFORMATION FOR SEQ ID NO: 134:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

TGCTGCTATG CCTCATCTTC

20

(2) INFORMATION FOR SEQ ID NO: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CARAGACAAA AGAAAATTGG

20

(2) INFORMATION FOR SEQ ID NO: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

CTATGGATGG AAATTGC

17

(2) INFORMATION FOR SEQ ID NO: 137:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CCTATGGATG GAAATTG

17

(2) INFORMATION FOR SEQ ID NO: 138:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

ACCTATGGAT GGAAATT

17

(2) INFORMATION FOR SEQ ID NO: 139:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

CTCAAGGCCAA CTCTATGTGG

20

(2) INFORMATION FOR SEQ ID NO: 140:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

CTCAAGGCAA CTCTATGGG

19

(2) INFORMATION FOR SEQ ID NO: 141:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

TCAAGGCAAC TCTATGTTG

19

(2) INFORMATION FOR SEQ ID NO: 142:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

ATCCCATCAT CTTGGG

16

(2) INFORMATION FOR SEQ ID NO: 143:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

ATCCCCATCAT CTTGGGCAG

19

(2) INFORMATION FOR SEQ ID NO: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

TCCCCATCATC TTGGGCAG

18

(2) INFORMATION FOR SEQ ID NO: 145:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

CCCATCATCT TGGGCTGG

18

(2) INFORMATION FOR SEQ ID NO: 146:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

TTCGCAAAAT ACCTATGG

18

(2) INFORMATION FOR SEQ ID NO: 147:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

TTTCGCAAAA TACCTATG

18

(2) INFORMATION FOR SEQ ID NO: 148:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

CTTTCGCAAA ATACCTATG

19

(2) INFORMATION FOR SEQ ID NO: 149:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

TCCCAAAATA CCTATGGG

18

(2) INFORMATION FOR SEQ ID NO: 150:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

TCTACTTCCA GGAACAT

17

(2) INFORMATION FOR SEQ ID NO: 151:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

TCTACTTCCA GGAACATC

18

(2) INFORMATION FOR SEQ ID NO: 152:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

CTCTACTTCC AGGAACAT

18

(2) INFORMATION FOR SEQ ID NO: 153:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

CTCTACTTCC AGGAACAG

18

(2) INFORMATION FOR SEQ ID NO: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

CTGCACGATT CCTGCT

16

(2) INFORMATION FOR SEQ ID NO: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

TGCACGATTC CTGCTCA

17

(2) INFORMATION FOR SEQ ID NO: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

CTGCACGATT CCTGCTC

17

(2) INFORMATION FOR SEQ ID NO: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

TGCACGATTC CTGCTCAA

18

(2) INFORMATION FOR SEQ ID NO: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

TTCGCAAGAT TCCTATG

17

(2) INFORMATION FOR SEQ ID NO: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

CTTTCGCAAG ATTCCAT

18

(2) INFORMATION FOR SEQ ID NO: 160:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CTTTCGCAAG ATTCCATA

17

(2) INFORMATION FOR SEQ ID NO: 161:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

CTTTCGCAAG ATTCCATATG

19

(2) INFORMATION FOR SEQ ID NO: 162:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

CTCTATGTAT CCCTCCT

17

(2) INFORMATION FOR SEQ ID NO: 163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

TCTATGTATC CCTCCTG

17

(2) INFORMATION FOR SEQ ID NO: 164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

CTCTATGTAT CCCTCCTGG

19

(2) INFORMATION FOR SEQ ID NO: 165:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

CCTCTATGTAT TCCCTCCT

18

(2) INFORMATION FOR SEQ ID NO: 166:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

CTGTACCAAA CCTTCGG

17

(2) INFORMATION FOR SEQ ID NO: 167:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

CTGTACCAAA CCTTCG

16

(2) INFORMATION FOR SEQ ID NO: 168:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

GCTGTACCAA ACCTTCGG

18

(2) INFORMATION FOR SEQ ID NO: 169:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

TGTACCAAAAC CTTCGGAG

18

(2) INFORMATION FOR SEQ ID NO: 170:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

GGACCCTGCC GAACCT

16

(2) INFORMATION FOR SEQ ID NO: 171:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

GGACCCTGCC GAACCG

16

(2) INFORMATION FOR SEQ ID NO: 172:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 15 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

GGGACCCTGC CGAAC

15

(2) INFORMATION FOR SEQ ID NO: 173:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 14 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

GGACCCCTGCC GAAC

14

(2) INFORMATION FOR SEQ ID NO: 174:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

GTTGCTGTTC AAAACCTT

18

(2) INFORMATION FOR SEQ ID NO: 175:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GTTGCTGTTC AAAACCTG

18

(2) INFORMATION FOR SEQ ID NO: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

TGTTGCTGTT CAAAACCTG

19

(2) INFORMATION FOR SEQ ID NO: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

ATGTTGCTGT TCAAAACCTG

20

(2) INFORMATION FOR SEQ ID NO: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

GATCCACGAC CACCA

15

(2) INFORMATION FOR SEQ ID NO: 179:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

GGATCCACGA CCACCA

16

(2) INFORMATION FOR SEQ ID NO: 180:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 15 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

GGATCCACGA CCACC

15

(2) INFORMATION FOR SEQ ID NO: 181:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

GATCCACGAC CACCAAG

17

(2) INFORMATION FOR SEQ ID NO: 182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TGTTCCAAAC CCTCGG

16

(2) INFORMATION FOR SEQ ID NO: 183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

CTGTTCCAAA CCCTCG

16

(2) INFORMATION FOR SEQ ID NO: 184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

CTGTTCCAAA CCCTCGG

17

(2) INFORMATION FOR SEQ ID NO: 185:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 185:

GTTCCAAACC CTCGGAT

17

(2) INFORMATION FOR SEQ ID NO: 186:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 186:

GCCAAATCTG TGCAGC

16

(2) INFORMATION FOR SEQ ID NO: 187:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 187:

CCAAATCTGT GCAGCAT

17

(2) INFORMATION FOR SEQ ID NO: 188:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 188:

GCCAAATCTG TGCAGCAG

18

(2) INFORMATION FOR SEQ ID NO: 189:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 189:

GGCCAATCT GTGCAGC

17

(2) INFORMATION FOR SEQ ID NO: 190:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 190:

ATCAAACAACA ACCAGTA

17

(2) INFORMATION FOR SEQ ID NO: 191:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs  
(B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 191:

GATCAACAAAC AACCAGT

17

(2) INFORMATION FOR SEQ ID NO: 192:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 192:

GATCAACAAAC AACCAGTA

18

(2) INFORMATION FOR SEQ ID NO: 193:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 193:

GGATCAACAA CAACCAGT

18

(2) INFORMATION FOR SEQ ID NO: 194:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 194:

TCAAGGCAAC TCTATGTGG

19

(2) INFORMATION FOR SEQ ID NO: 195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 195:

AGGTTAAAGG TCTTTGT

17

(2) INFORMATION FOR SEQ ID NO: 196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 196:

TAGGTTAAAG GTCTTTGG

18

(2) INFORMATION FOR SEQ ID NO: 197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 197:

TTAGGTTAAA GGTCTTT

17

(2) INFORMATION FOR SEQ ID NO: 198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 198:

GGTTAAAGGT CTTTGTAGG

19

(2) INFORMATION FOR SEQ ID NO: 199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 199:

AGGTTAACATGA TCTTTGT

17

(2) INFORMATION FOR SEQ ID NO: 200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 200:

TAGGTTAATG ATCTTTGG

18

(2) INFORMATION FOR SEQ ID NO: 201:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 201:

CTTTCCGAAG ATTCCTATGG

20

(2) INFORMATION FOR SEQ ID NO: 202:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 202:

GCTTTCGCAA GATTCTATG

20

(2) INFORMATION FOR SEQ ID NO: 203:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 203:

GCTTCGCAA GATTCTATG G

21

(2) INFORMATION FOR SEQ ID NO: 204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 204:

CTTTCGCAAG ATTCTATGG G

21

(2) INFORMATION FOR SEQ ID NO: 205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 205:

GCTGTACCAA ACCTTCGGAG

20

(2) INFORMATION FOR SEQ ID NO: 206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 206:

TGCTGTACCA AACCTTCGG

19

(2) INFORMATION FOR SEQ ID NO: 207:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 21 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 207:

TGCTGTACCA AACCTTCGGA G

21

(2) INFORMATION FOR SEQ ID NO: 208:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 208:

GCTGTACCAA ACCTTCGGAT

20

(2) INFORMATION FOR SEQ ID NO: 209:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 16 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)  
(iii) HYPOTHETICAL: NO  
(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 209:

TGGTTCGCCG GGCTTT

16

(2) INFORMATION FOR SEQ ID NO: 210:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 17 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 210:

GTGGTTCGCC GGGCTTG

17

(2) INFORMATION FOR SEQ ID NO: 211:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 211:

GGTTCGCCGG GCTTTC

16

(2) INFORMATION FOR SEQ ID NO: 212:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 212:

TGGTTCGCCG GGCTTTC

17

(2) INFORMATION FOR SEQ ID NO: 213:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 213:

AGTGGTTCGC CGGGCTGG

18

(2) INFORMATION FOR SEQ ID NO: 214:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 214:

AGGATCCACG ACCACCAGG

19

(2) INFORMATION FOR SEQ ID NO: 215:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 215:

AGGATCCACG ACCACCAGT

19

(2) INFORMATION FOR SEQ ID NO: 216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 216:

CAGGATCCAC GACCACCAGG

20

(2) INFORMATION FOR SEQ ID NO: 217:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 217:

CTGTTCCAAA CCCTCGGAG

19

(2) INFORMATION FOR SEQ ID NO: 218:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 218:

CTGTTCCAAA CCCTCGGAT

19

(2) INFORMATION FOR SEQ ID NO: 219:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 219:

GCTGTTCCAA ACCCTCGAG

20

(2) INFORMATION FOR SEQ ID NO: 220:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 220:

CTGAACCTTT ACCCCGTTGC

20

(2) INFORMATION FOR SEQ ID NO: 221:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 221:

CTCGCCAAT TACAAGGCCT TTC

23

(2) INFORMATION FOR SEQ ID NO: 222:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 222:

AGAATGGCTT GCCTGAGTGC

20

(2) INFORMATION FOR SEQ ID NO: 223:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 223:

GCTTTCGCAA GATTCTATG GG

22

(2) INFORMATION FOR SEQ ID NO: 224:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 224:

GGCTTCGCA AGATTCTAT GG

22

(2) INFORMATION FOR SEQ ID NO: 225:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 225:

GGCTTCGCA AGATTCTAT GGG.

23

(2) INFORMATION FOR SEQ ID NO: 226:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 226:

GGCTTCGCA AGATTCTAT GGGA

24

(2) INFORMATION FOR SEQ ID NO: 227:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 227:

CAGCTATATG GATGATGTG

19

(2) INFORMATION FOR SEQ ID NO: 228:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 228:

AGCTATATGG ATGATGTGGG

20

(2) INFORMATION FOR SEQ ID NO: 229:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 229:

GCTATATGGA TGATGTGGT

19

(2) INFORMATION FOR SEQ ID NO: 230:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 230:

AGCTATATGG ATGATGTGGT

20

(2) INFORMATION FOR SEQ ID NO: 231:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 19 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 231:

CAGCTATATG GATGATATA

19

(2) INFORMATION FOR SEQ ID NO: 232:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 20 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 232:

AGCTATATGG ATGATATAAGT

20

(2) INFORMATION FOR SEQ ID NO: 233:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 19 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 233:

GCTATATGGA TGATATAGT

19

(2) INFORMATION FOR SEQ ID NO: 234:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 20 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 234:

AGCTATATGG ATGATATAAGT

20

(2) INFORMATION FOR SEQ ID NO: 235:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 17 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 235:

CCATCATCTT GGGCTTG

17

(2) INFORMATION FOR SEQ ID NO: 236:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 236:

CATCATCTTG GGCTTT

16

(2) INFORMATION FOR SEQ ID NO: 237:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 237:

CCATCATCTT GGGCTTT

17

(2) INFORMATION FOR SEQ ID NO: 238:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 238:

CCATCATCTT GGGCTTTC

18

(2) INFORMATION FOR SEQ ID NO: 239:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 239:

CCCACTGTCT GGCTTTC

17

(2) INFORMATION FOR SEQ ID NO: 240:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 240:

CCACTGTCTG GCTTTC

16

(2) INFORMATION FOR SEQ ID NO: 241:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 15 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 241:

CCACTGTCTG GCTTT

15

(2) INFORMATION FOR SEQ ID NO: 242:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 16 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 242:

CCCACTGTCT GGCTTG

16

(2) INFORMATION FOR SEQ ID NO: 243:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 243:

TATATGGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 244:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 244:

TATGTGGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 245:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 245:

TATATAGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 246:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 246:

TATATTGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 247:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 247:

TATGTAGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 248:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 248:

TATGTTGATG ATGTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 249:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 249:

TATATGGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 250:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 250:

TATATGGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 251:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 251:

TATGTGGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 252:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 252:

TATGTGGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 253:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 253:

TATATAGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 254:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 254:

TATATAGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 255:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 255:

TATATTGATG ATATAGTA

18

(2) INFORMATION FOR SEQ ID NO: 256:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 256:

TATATTGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 257:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 257:

TATGTAGATG ATATACTA

18

(2) INFORMATION FOR SEQ ID NO: 258:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 258:

TATGTAGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 259:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 259:

TATGTTGATG ATATACTA

18

(2) INFORMATION FOR SEQ ID NO: 260:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 260:

TATGTTGATG ATATCGTA

18

(2) INFORMATION FOR SEQ ID NO: 261:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 261:

TATATGGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 262:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 262:

TATGTGGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 263:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 263:

TATATAGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 264:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 264:

TATATTGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 265:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 265:

TATGTAGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 266:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 266:

TATGTTGATG ATCTGGTA

18

(2) INFORMATION FOR SEQ ID NO: 267:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 267:

TATGGGAGTG GGCTCAG

18

(2) INFORMATION FOR SEQ ID NO: 268:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 268:

TATGGGATTG GGCTCAG

18

(2) INFORMATION FOR SEQ ID NO: 269:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 18 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 269:

CAGTCCGTTT CTCTTGGC

18

(2) INFORMATION FOR SEQ ID NO: 270:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 270:

CAGTCTGTTT CTCTTGCG

18

(2) INFORMATION FOR SEQ ID NO: 271:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 271:

CAGTCCGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 272:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 272:

CAGTCTGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 273:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 18 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 273:

CAGTCCGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 274:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 274:

CAGTCTGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 275:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 275:

CAGCCCCGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 276:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 276:

CAGCCTGTTT CTCCTGGC

18

(2) INFORMATION FOR SEQ ID NO: 277:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 277:

CAGCCCGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 278:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 278:

CAGCCTGTTT CTCATGGC

18

(2) INFORMATION FOR SEQ ID NO: 279:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 279:

AATTCCACTG	CCTTCCACCA	AGCTCTGCAG	GATCCCAAAG	TCAGGGGTCT	GTATCTTCT	60
GCTGGTGGCT	CCAGTTCA	GG AACAGTAAAC	CCTGCTCCGA	ATATTGCCTC	TCACATCTCG	120
TCAATCTCCG	CGAGGACTGG	GGACCTGTG	ACGAACATGG	AGAACATCAC	ATCAGGATT	180
CTAGGACCCC	TGCTCGTGT	TT ACAGGGGGG	TTTTCTTGT	TGACAAGAAT	CCTCACAATA	240
CCGCAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGGTC	ACCCGTGTGT	300
CTTGGCCAAA	ATT CGCAGTC	CCC AACCTCC	AATCACTCAC	CAACCTCCTG	TCCTCCAATT	360
TGT CCTGGTT	ATCGCTGGAT	GTGTCTGCCG	CGTTTATCA	TATT CCTCTT	CATCCTGCTG	420
CTATGCCCTCA	TCTTCTTGT	GGTTCTCTG	GATTATCAAG	GTATGTTGCC	CGTTTGTCC	480
CTAATTCCAG	GATCAACAAC	AACCAGTACG	GGACCATGCA	AAACCTGCAC	GA CTCCTGCT	540
CAAGGCAACT	CTATGTTCC	CTCATGTTGC	TGTACAAAAC	CTACGGATGG	AAATTGCACC	600
TGTATTCCCA	TCCC ATCGTC	CTGGGCTTTC	GCAAAATACC	TATGGGAGTG	GGCCTCAGTC	660
CGTTTCTCTT	GGCTCAGTT	ACTAGTGCCA	TTT GTTCAGT	GGTTCGTAGG	GCTTCCCCC	720
ACTGTTGGC	TTTCAGCTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGACT	GTACAGCATE	780
GTGAGTCCCT	TTATACCGCT	GTTACCAATT	TTCTTTGTC	TCTGGGTATA	CATT TAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTATTCCC	TAAACTTCAT	GGTCTACATA	ATTGGAAGTT	900
GGGAACATT	GCCACAGGAT	CATATTGTAC	AAAAGATCAA	ACACTGTTT	AGAAAACCTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GTCAAAGAAT	TGTGGTCTT	TTGGGCTT	1020
CTGCTCCATT	TACTCAATGT	GGATATCCTG	CCTTAATGCC	TTTGTATGCA	TGTATAACAG	1080
CTAACACAGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTAAGTAAA	CAGTACATGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGCCCTG	GTCTGTGCCA	AGTGTGCT	GACGCCAACCC	1200
CCACTGGCTG	GGGCTTGGCC	ATAGGCCATC	AGCGCATGCG	TGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTGTTGC	TCGCAGCCGG	TCTGGAGCAA	1320
AGCTCATCGG	AACTGACAAT	TCTGTCGTCC	TCTCGCGGAA	ATATACATCG	TTTCCATGGC	1380
TGCTAGGCTG	TACTGCCAAC	TGGATCCTTC	GGGGGACGTC	CTTTGTTAC	GTCCC GTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCTCGGG	GGCGCTTGGG	AGTCTCTCGT	CCCCTTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTCA	GGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTGT	CTTCACCTCT	GCACGTTGCA	TGGAGACCAC	1620
CGTGAACGCC	CATCAGATCC	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GA CTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTAAGG	ACTGGGAGGA	1740
GCTGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCCGACCA	GCACCATGCA	ACTTTTCAC	CTCTGCC TAA	TCATCTCTTG	TACATGTCCC	1860

ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTG GAGCTACTGT GGAGTTACTC TCGTTTTGC CTTCTGACTT CTTTCCTTCC	1980
GTCAGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGAG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAAC TGCACTCAGG CAAGCCATTC TCTGCTGGGT GGAATTGATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTG GAAGATCCAG CATCCAGGGA TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGTTAAAG ATCAGGCAAC TATTGTGGTT TCATATATCT	2220
TGCCCTACTT TTGGAAGAGA GACTGTGCTT GAATATTG TCTCTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGGGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACCCAGAT CTCAATGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCCTGG ACTCATAAGG TGGGAAACTT TACTGGGCTT TATTCCCTCA CAGTACCTAT	2520
CTTTAACCTT GAATGGCAAA CTCCTCCTT TCCTAAGATT CATTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTG TGGGCCCTCT CACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCCAGATTCT ATCCTACCCA CACTAAATAT TTGCCCTTAG ACAAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ATTATTTACA	2760
TACTCTTGG AAGGCTGGTA TTCTATATAA GAGGGAAACC ACACGTAGCG CATCATTG	2820
CGGGTCACCA TATTCTTGGG AACAAAGAGCT ACAGCATGGG AGGTTGGTCA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAT CTTCTGTTC CCAACCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGCATTCGGA GCCAACTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCAGCAGCC AACCAAGGTAG GAGTGGGAGC ATTGGGCCA AGGCTCACCC	3060
CTCCACACGG CGGTATTTG GGGTGGAGCC CTCAGGCTCA GGGCATATTG ACCACAGTGT	3120
CAACAATTCC TCCTCCTGCC TCCACCAATC GGCAAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT AAGAGACAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 280:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3200 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 280:

AATTCCACTG CCTTGCACCA AGCTCTGCAG GATCCCAGAG TCAGGGGTCT GTATCTTCT

GCTGGTGGCT	CCAGTTCA	G	AACAGTAAAC	CCTGCTCCGA	ATATTGCCTC	TCACATCTCG	120
TCAATCTCCG	CGAGGACTGG	GGACCCCTGTG	ACGATCATGG	AGAACATCAC	ATCAGGATTC		180
CTAGGACCCC	TGCTCGTGT	TT	ACAGGCCGGG	TTTTCTTGT	TGACAAGAAT	CCTCACAAATA	240
CCGCAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGGATC	ACCCGTGTGT		300
CTTGGCCAAA	ATTCGCAGTC	CCCAACCTCC	AATCACTCAC	CAACCTCCTG	TCCTCCAATT		360
TGTCCCTGGTT	ATCGCTGGAT	GTGTCTGCGG	CGTTTTATCA	TATTCCCTTT	CATCCTGCTG		420
CTATGCCTCA	TCTTCTTATT	GGTTCTTCTG	GATTATCAAG	GTATGTTGCC	CGTTTGTCC		480
CTAATTCCAG	GATCAACAAAC	AACCAGTACG	GGACCATGCA	AAACCTGCAC	GACTCCTGCT		540
CAAGGCAACT	CTAAGTTCC	CTCATGTTGC	TGTACAAAAC	CTACGGATGG	AAATTGCACC		600
TGTATTCCCA	TCCCATCGTC	CTGGGCTTTC	GCAAAATACC	TATGGGAGTG	GGCCTCAGTC		660
CGTTTCTCTT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTCGTAGG	GCTTCCCCC		720
ACTGTTGGC	TTTCAGCTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATE		780
GTGAGTCCCT	TTATAACCGCT	GTTACCAATT	TTCTTTGTC	TCTGGGTATA	CATTTAAACC		840
CTAACAAAAC	AAAAAGATGG	GGTTATTCCC	TAAACATTCA	GGGCTACATA	ATTGGAAGTT		900
GGGAACTTT	GCCACAGGAT	CATATTGTAC	AAAAGATCAA	ACACTGTTT	AGAAAACCTC		960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GTCAAAGAAT	TGTGGGTCTT	TTGGGCTTTG		1020
CTGCTCCATT	TACACAATGT	GGATATCCTG	CCTTAATGCC	TTTGTATGCA	TGTATACAAG		1080
CTAACACAGG	TTTCACTTTC	TCGCCAACTT	ACAAGGCCCTT	TCTAAGTAAA	CACTACATGA		1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTGTGTTGCT	GACGCAACCC		1200
CCACTGGCTG	GGGCTTAGCC	ATAGGCCATC	AGCGCATGCG	TGGAACCTTT	GTGGCTCCTC		1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTGTTGC	TCGCAGCCGG	TCTGGAGCAA		1320
AGCTCATCGG	AACTGACAAT	TCTGTCGTCC	TCTCGCGGAA	ATATAACATCA	TTTCCATGGC		1380
TGCTAGGCTG	TACTGCCAAC	TGGATCCTTC	GCAGGGACGTC	CTTTGTTTAC	GTCCCGTCTGG		1440
CGCTGAATCC	CGCGGACGAC	CCCTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCTTCTCC		1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC		1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTCG	CTTCACCTCT	GCACGTTGCA	TGGCGACCAC		1620
CGTGAACGCC	CATCAGATCC	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCCCAGC		1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTTAAGG	ACTGGGAGGA		1740
GTTGGGGAG	GAGATTAGGT	TAATGATCTT	TGTATTAGGA	GGCTGTAGGC	ATAAATTGGT		1800
CTGGCCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCCTAA	TCATCTCTTG	TACATGTCCC		1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCCTGGG	TGGCTTGGG	GCATGGACAT	TGACCCCTTAT		1920
AAAGAATTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTGC	CTTCTGACTT	CTTTCCTTCC		1980
GTACGAGATC	TCCTAGACAC	CGCCTCAGCT	CTGTATCGAG	AAGCCTTAGA	GTCTCCTGAG		2040

CATTGCTCAC CTCACCATAAC TGCACTCAGG CAAGCCATTC TCTGCTGGGG GGAATTGATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTTG CAAGATCCAG CATCCAGAGA TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGTTAAAG ATCAGGCAAC TATTGTGGTT TCATATATCT	2220
TGCCCTTACTT TTGGAAGAGA GACTGTACTT GAATATTGG TCTCTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGGGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCAATCGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCCTTGG ACTCATAAGG TCGGAAACTT TACGGGGCTT TATTCCCTCTA CAGTACCTAT	2520
CTTTAATCCT GAATGGCAAAT CTCCTTCCTT TCCTAAGATT CATTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTG TGGGCCCTCT CACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCTAGATTCT ATCCTACCCA CACTAAATAT TTGCCCTTAG ACAAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ATTATTACAT	2760
TACTCTTTGG AAGGCTGGTA TTCTATATAA GAGGGAAACC ACACGTAGCG CATCATTTG	2820
CGGGTCACCA TATTCTTGGG AACAAAGAGCT ACAGCATTG CAAAGGCATG GGGACGAATC	2880
TTTCTGTTCC CAACCCCTCTG GGATTCCCTTC CCGATCATCA GTTGGACCCCT GCATTGGAG	2940
CCAACCTAAC AAATCCAGAT TGGGACTTCA ACCCCATCAA GGACCACTGG CCAGCAGCCA	3000
ACCAGGTAGG AGTGGGAGCA TTGGGCCAG GGCTCACCCCC TCCACACGGC GGTATTTGG	3060
GGTGGAGCCC TCAGGCTCAG GGCATATTGA CCACAGTGTC AACAAATTCT CCTCCTGCCT	3120
CCACCAATCG GCAGTCAGGA AGGCAGCCTA CTCCCATCTC TCCACCTCTA AGAGACAGTC	3180
ATCCTCAGGC CATGCAGTGG	3200

(2) INFORMATION FOR SEQ ID NO: 281:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3221 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 281:

AATTCCACTG CCTTCCACCA AGCTCTGCAA GACCCAGAG TCAGGGGTCT GTATTTCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGCTCCGA ATATTGCCTC TCACATCTCG	120
TCAATCTCCG CGAGGACCGG GGACCCGTG ACGAACATGG AGAACATCAC ATCAGGATTC	180

CTAGGACCCC	TGCCCGTGT	ACAGGGGGGG	TTTTCTTGT	TGACAAGAAT	CCTCACAATA	240
CCGCAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGGATC	ACCCGTGTGT	300
CTTGGCCAAA	ATTCGCGATC	CCCAACCTCC	AATCACTCAC	CAACCTCCTG	TCCTCCAATT	360
TGTCCTGGTT	ATCGCTGGAT	GTGTCTGCGG	CGTTTTATCA	TATTCTCTT	CATCCTGCTG	420
CTATGCCTCA	TCTTCTTATT	GGTTCTCTG	GATTATCAAG	GTATGTTGCC	CGTTTGTCT	480
CTAATTCTAG	GATCAACAAAC	AACCAGTACG	GGACCATGCA	AAACCTGCAC	GAECTCCTGCT	540
CAAGGCAACT	CTATGTTCC	CTCATGTTGC	TGTACAAAAC	CTACGGATGG	AAATTGCACC	600
TGTATTCCCA	TCCCATCGTC	TTGGGCTTTC	GCAAAATACC	TATGGGAGTG	GGCCTCAGTC	660
CGTTTCTCTT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTCGTAGG	GCTTTCCCCC	720
ACTGTTTGGC	TTTCAGCTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATE	780
GTGAGTTCCCT	TTATACCGCT	GTTACCAATT	TTCTTTGTC	TCTGGGTATA	CATTAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTATTCCC	AAAACCTCAT	GGGTTATGTA	ATTGGAAGTT	900
GGGGAACATT	GCCACAGGAT	CATATTGTAC	AAAAAATCAA	ACACTGTTTT	AGAAAACCTTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GTCAAAGAAT	TGTGGGTCTT	TTGGGCTTTG	1020
CTGCTCCTTT	TACACAATGT	GGATATCCTG	CCTTAATGCC	CTTGTATGCC	TGTATACAAG	1080
CTAAACAGGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTAAGTAAA	CAGTACATGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTATTGCT	GATGCAACCC	1200
CCACTGGCTG	GGGCTTGGCC	ATAGGCCATC	AGCGCATGCG	CGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTGTTGC	TCGCAGCCGG	TCTGGAGCGA	1320
AACTCATCGG	AACTGACAAT	TCTGCGTCC	TCTCGCGGAA	ATATACCTCG	TTTCCATGGC	1380
TAATAGGCTG	TGCTGCCAAC	TGGATCCTTC	GCGGGACGTC	CTTTGTTAC	GTCCCCTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCCTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACCTCG	CTTCACCTCT	GCACGTTGCC	TGGAGACCAC	1620
CGTGAACGCC	CATCAGATCC	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCCCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTTAAGG	ACTGGGAGGA	1740
GCTGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCTAA	TCATCTCTTG	TACATGTCCC	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCCTGGG	TGGCTTGGG	GCATGGACAT	TGACCCTTAT	1920
AAAGAATTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTGC	CTTCTGACTT	CTTTCTTCC	1980
GTCAGAGATC	TCCTAGACAC	CGCCTCGGCT	CTGTATCGGG	AAGCCTTAGA	GTCTCCTGAG	2040
CATTGCTCAC	CTCACCATAC	CGCACTCAGG	CAAGCCATTC	TCTGCTGGGG	GGAATTGATG	2100
ACTCTAGCTA	CCTGGGTGGG	TAATAATTG	GAAGATCCAG	CATCCAGGG	TCTAGTAGTC	2160
AATTATGTTA	ATACTAACAT	GGGATTAAAG	ATCAGGCAAC	TCTTGTGGTT	TCATATCTCT	2220

TGCCTTACTT TTGGAAGAGA AACTGTACTT GAATATTTGG TCTCTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGGGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCATCGCC GCGTCGCAGA AGATCTCAAT CTCGGAAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TGGGAAACTT CACTGGGCTT TATTCCCTTA CAGCACCTAT	2520
CTTTAACCTT GAATGGCAA CTCCTTCCTT TCCTAAAATT CATTTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTG TGGGCCCTCT CACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCTAGATTCT ATCCTACCCA CACTAAATAT TTGCCCTTAG ACAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ATTATTTACA	2760
TACTCTTGG AAGGCGGGTA TTCTATATAA GAGAGAAACC ACACGTAGCG CATCATTTG	2820
CGGGTCACCA TATTCTTGGG AACAAAGAGCT ACAGCATGGG AGGTTGGTCA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAT CTTCTGTTC CCAACCCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGTATTGGA GCCAACTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCAGCAGCC AACCAAGGTAG GAGTGGGAGC ATTGGGCCA GGGTCACCC	3060
CTCCACACGG CGGTGTTTG GGGTGGAGCC CTCAGGCTCA GGGCATGTTG ACCCCAGTGT	3120
CAACAATTCC TCCCTCTGCC TCCGCCAATC GGCAAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT AAGAGACAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 282:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3221 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 282:

AATTCCACTG CCTTCCACCA AGCTCTGCAG GATCCCAGAG TCAGGGGTCT GTATCTTCCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGCTCCGA ATATTGCCTC TCACATCTCG	120
TCAATCTCCG CGAGGACTGG GGACCCGTG ACAGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGGGGG TTTTCCCTGT TGACAAGAAT CCTCACAAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGTC ACCCGTGTGC	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360

TGTCCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTATT GGTTCTTCTG GATTATCAAG GTATGTTGCC CGTTTGTCTT	480
ATAATTCCAG GATCAACAAAC AACCAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTTTGTTTC CTCATGTTGC TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCCA TCCCCATCGTC CTGGGCTTTC GCAAATACC TATGGGAGCG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTGGC TTTTAGCTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGGCATC	780
GTGAGGCCCT TTATACCGCT GTTACCAATT TTCTTTGTC TCTGGGTATA CATTAAACC	840
CTAACAAAAC AAAAAGATGG GGTTATTCCC TAAACTTCAT GGGTTACAGA ATTGGAAGTT	900
GGGGAACATT GCCACAGGAT CACATTGTAC AAAAGATCAA ACACTGTTT AGAAAACCTC	960
CTGTTAACAG GCCTATTGAT TGGAAGGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCTCCTTT TACACAATGT GGATATCCTG CCTTAATGCC TTTGTATGCA TGTATACAAG	1080
CTAAACAGGC TTTCTCTTC TCGCCAACCTT ACAAGGCCTT TCTAAGTAAA CAGTACCTGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCTG GTCTGTGCCA AGTGTGCTT GACGCAACCC	1200
CCACTGGCTG GGGCTTAGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTGTC TCGCAGCCGG TCTGGAGCAA	1320
AGCTCATCGG AACTGACAAT TCTGTCGTCC TCTCGCGGAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTTC GCGGGACGTC CTTGTTTAC GTCCCGTCTGG	1440
CGCTGAATCC CGCGGACGAC CCCTCTCGGG GCCGCTTGGG ACTCTATCGT CCCCTCTCC	1500
GTCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTCACCTCT GCACGTTGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGAGCC TGCCCAAGGT CTTACATAAG AGAACTCTTG GACTCCCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTAAGG ACTGGGAGGA	1740
GCTGGGGAG GAGATTAGGT TAATGATCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTCAC CTCTGCCCTAA TCATCTCTTG TTCATGTCTC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGAG GCATGGACAT TGACCCCTAT	1920
AAAGAATTG GAGCTAGTGT GGAGTTACTC TCGTTTTGTC CTCATGACTT CTTTCCTTCC	1980
GTCAGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGAG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAAC TGCACTCAGG CAAGCCGTC TCTGCTGGGG GGAATTAAATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTG CAAGATCCAG CATCCAGGGA TCAAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGTTAAAG ATCAGGCAAC TATTGTGGTT TCATATATCT	2220
TGTCTTATGT TTGGAAGAGA CACTGTACTT GAATATTGG TCTCTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCCTATAG ACCACCAAAT GCCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GATGTCGGGA CCGACGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400

AGACGCAGAT CTCAATGCC GCGTCGAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCCTTGG ACTCATAAGG TGGGAAACTT TACTGGGCTT TATTCCCTCTA CAGTACCTAT	2520
CTTTAACCTT GAATGGCAAA CTCCTTCCTT TCCTAAGATT CATTACAAG AGGACATTAT	2580
TAATAGGTGT CAACAATTTG TGGGCCCTCT TACTGTAAAT GAAAAGAGAA GATTGAAATT	2640
AATTATGCCT GCTAGATTCT ATCCTACCCA CACAAAATAT TTGCCCTTAG ACAAAAGGAAT	2700
TAAACCTTAT TATCCAGATC AGGTAGTTAA TCATTACTTC CAAACCAGAC ACTATTTACA	2760
TACTCTTGG AAGGCTGGTA TTCTATATAA GAGGGAACCC ACACGTAGCG CATCATTTC	2820
CCGGTCACCA TATTCTTGGG AACAAAGAGCT ACAGCATGGG AGGTGGGACA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAT CTTTCTGTT CCAACCCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTCCACCC TGCAATTGGA GCCAACTCAA ACAATCCAGA TTGGGACTTC AACCCCCATCA	3000
AGGACCACTG GCCAGCAGCC AACCAAGGTGG GAGTGGGAGC ATTGGGGCCA GGGCTCACCC	3060
CTCCACACGG CGGTATTTTG GGGTGGAGCC CTCAGGCTCA AGGCATATTG ACCACAGTGT	3120
CAACAATTCC TCCTCCTGCC TCCACCAATC GGCAAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT GAGAGAAAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 283:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3221 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 283:

AATTCCACAG CTTTCCACCA AGCTCTGCAA GATCCCAGAG TCAGGGGCCT GTATTTCT	60
GCTGGTGGCT CCAGTCAGG AACACTCAAC CCTGTTCCAA CTATTGCCCTC TCACATCTCG	120
TCAATCTCCT CGAGGATTGG GGACCCCTGCA CCGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGTGTT ACAGGGGGGG TTTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTATT GGTTCTCTG GATTATCAAG GTATGTTGCC CGTTTGTCT	480
CTAATTCCAG GATCAACAAAC AACCAAGCACG GGACCCCTGCA AAACCTGCAC GACTCCTGCT	540

CAAGGCAACT CTATGTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AAATTGCACC	600
TGTATTCCA TCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGCTAT ATGGATGATG TGGTACTGGG GCCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACCC	840
CTAACAAAAC AAAGAGATGG GGTTATTCCC TGAATTTCAT GGGTTATGTA ATTGGAAAGTT	900
GGGGTACATT GCCCACAGGAT CATATTGTAC AAAAAATCAA ACACGTGTTT AGAAAACCTTC	960
CTGTTAATCG ACCTATTGAT TGGAAAGTAT GTCAGAGACT TGTAGGTCTT TTAGGCTTG	1020
CCGCTCCATT TACACAATGT GGTTACCTG CATTAATGCC TTTGTATGCA TGTATACAAG	1080
CGAACACAGGC TTTTACTTTC TCGCCAACCTT ACAAGGCCTT TCTAAGTAAA CAGTATATGA	1140
ACCTTTACCC CGTTGCCCGG CAACGCCCTG GTCTGTGCCA AGTGTGTTGCT GACGCCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATCGGCCATC AGCGCATGCG TGAAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCAGAA CTCCTAGCCG CTTGTTTGCT TCGCAGCCGG TCTGGAGCAA	1320
AACTCATCGG GACTGACAAT TCTGTCGTCC TTTCTCAGAA ATATACATCC TTTCCATAGC	1380
TGCTAGGTTG TACTGCCAAC TAGATTCTTC GCAGGGACGTC CTTTGTCTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCGCGAG GCCGCTTGGG ACTGTATCGT CCCCTCTCC	1500
GTCTGCCGTA CCGTCCGACC ACGGGGCGCA CCTCTCTTAA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACCTCG CTTCACCTCT GCACGTTGCA TGGAGACCAC	1620
CGTGAACGCC CATCAGGTCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTAAAG ACTGGGAGGAA	1740
GTTGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA TTATCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCTTG TACATGTCCC	1860
ACTTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCCTTAT	1920
AAAGAATTG AGCTACTGTG GAGTTACTCT CATTGTTGCT TTCTGACTTC TTTCCTTCCG	1980
TCCGGGATCT ACTAGAATAC AGCCTCAGCT CTATATCGGG AAGCCTTAGA GTCTCCTGAG	2040
CATTGCTCAC CTCACCATAAC AGCACTCAGG CAAGCCATTG TCTGCTGGGG GAAATTAATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTG GAAGATCCAG CATCCAGGG TCTAGTAGTC	2160
AATTATGTTA ATACTAACAT GGGCCTAAAG ATCAGGCAAT TATTGTGGTT TCATATTCT	2220
TGCCTTACTT TTGGAAGAGA AACTGTCCTT GAGTATTG TCTCTTCGG AGTGTGGATT	2280
CGCACTCCCTC CAGCCTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGA CCGAGGCAGG TCCCCTAGAA GAAGAACTCC CTCGCCTCGC	2400
AGACGCAGAT CTCATCGCC GCGTCGCAGA AGATCTCAAT CTCGGGAATC TCAATGTTAG	2460
TATTCTTGG ACTCATAAGG TGGGAAATT TACTGGGCTT TATTCTTCTA CTGTCCTAT	2520
CTTTAACCTT GAATGGCAAA CACCTTCTTT TCCTAAAATT CATTACATG AAGACATTGC	2580

TAATAGGTGT CAGCAATTG TAGGCCCTCT CACTGAAAT GAAAAAAGAA GACTGAAATT	2640
AATTATGCCT GCTAGGTTT ATCCTAACAG CACAAAATAT TTGCCCTTAG ACAAAGGGAT	2700
TAAAACTTAT TATCCTGATC ATGTAGTTAA TCATTACTTT CAAACCCGAC ATTATTTACA	2760
TACTCTTGG AAGGCTGGGA TTCTATATAA GAGGGAAACT ACACGTAGCG CCTCATTG	2820
CGGGTCACCA TATTCTTGGG AACAAAGAGCT ACATCATGGG AGGTTGGTCA TCAAAACCTC	2880
GCAAAGGCAT GGGGACGAAC CTTTCTGTTC CCAACCCTCT GGGATTCTTT CCCGATCATC	2940
AGTTGGACCC TGCATTCGGA GCCAATTCAA ACAATCCAGA TTGGGACTTC AACCCCATCA	3000
AGGACCACTG GCCACAAGCC AACCAAGGTAG GAGTGGGAGC ATTTGGGCCA GGGTTCACTC	3060
CCCCACACGG AGGTGTTTG GGGTGGAGCC CTCAGGCTCA GGGCATATTG GCCACCGTGC	3120
CAGCGATGCC TCCTCCTGCC TCCACCAATC GGCAAGTCAGG AAGGCAGCCT ACTCCCATCT	3180
CTCCACCTCT AAGAGACAGT CATCCTCAGG CCATGCAGTG G	3221

(2) INFORMATION FOR SEQ ID NO: 284:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:284:

AACTCCACCA CGTTCACCA AACTCTCAA GATCCCAGAG TCAGGGCTCT GTACTTCC	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGTTCAGA ACAC TGCTC TTCCATATCG	120
TCAATCTTAT CGACGACTGG GGACCCCTGTG CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGT ACAGGGGGGG TTTTCTCGT TGACAAAAT CCTCACAATA	240
CCTCTGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGAAAC ACCCGTGTGT	300
CTTGGCCAAA ATT CGCAGTC CCAAATCTCC AGTCACTCAC CAACTGTTG TCCTCCGATT	360
TGTCCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCCCTTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTG GGTTCTCTG GACTATCAAG GTATGTTGCC CGTTTGTCT	480
CTAATTCCAG GATCATCAAC CACCAGCACA GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTACAAAAC CTACGGACGG AAACTGCACC	600
TGTATTCCCA TCCCCTCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCTGAGG GCTTTCCCCC	720
ACTGTCTGGC TTTCAAGTTAT ATGGATGATG TGGTTTGGG GGCCAAGTCT GTACAACATC	780

TTGAGTCCCT TTATGCCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTCAGAAAAC AAAAAGATGG GGCTACTCCC TTAACTCAT GGGGTATGTA ATTGGAAAGTT	900
GGGGGACCTT ACCCCAAGAA CATATTGTGT TGAAAATCAA ACAATGTTT AGGAAACTTC	960
CTGTAAACAG GCCTATTGAT TGGAAAGTAT GTCAACGAAT TGTGGTCTT TTGGGATTTG	1020
CTGCTCCTTT CACACAATGT GGATATCCTG CTTAATGCC TTTATATGCA TGTATAACAAG	1080
CTAAACAGGC TTTTACTTTT TCGCCAACGT ATAAGGCCTT TCTAAACAAA CAATATCTGA	1140
ACCTTACCC CGTTGCTCGG CAACGCCAG GTCTGTGCCA AGTGTGCT GACGCCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATAGGCCATC AGCGCATGCG TGGGACCTTT GTGCTCCTC	1260
TGCCGATCCA TACTGTGGAA CTCCTAGCAG CTTGTTTGC TCGCAGCAGG TCTGGAGCAA	1320
AACTTATCGG GACTGACAAT TCTGTCGTC TTTCCCGCAA ATATACATCG TTTCCATGCC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTGTCCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCCCGGG GCCGCTTGGG GCTCTACCGC CCGCTTCTCC	1500
GCCTGCCGTA CCGTCCGACC ACGGGGCGCA CCTCTCTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACCTCG CTTCACCTCT GCACGTGCA TGGAGACCAC	1620
CGTGAACGCC CATCGGAACC TGCCCAAGGT CTTGCATAAG AGGACTCTTG GACTTTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCACACTT CAAAGACTGT GTGTTACTG AGTGGGAGGA	1740
GTTGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTGTCACTT CTTTCCTTCT	1980
ATTCGAGATC TTCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAC GGCACTCAGG CAAGCTATTG TGTGTTGGG TGAGTTGATG	2100
AATCTAGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CCTCCCGGA ATTAGTAGTC	2160
AGTTATGTCA ATGTTAATAT GGGCTAAAA ATCAGACAAAC TATTGTGGTT TCACATTCC	2220
TGTCTTACGT TTGGAAGAGA AACTGTTCTT GAATATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACACCTC CAGCATATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCT AGAAGAAGAA CTCCCTGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGAA ACTTACGGG GCTTTATTCT TCTACGGTAC CTAGCTTAA	2520
TCCTCAATGG CAAACTCCTT CATTCTGA CATTCAATTG CAGGAGGACA TCATTAATAA	2580
GTGTAAACAA TTTGTGGAC CCCTTACAGT GAATGAAAAA AGGAGACTAA AATTGATTAT	2640
GCCTGCTAGG TTCTATCCCA ATGTTACTAA ATATTTGCC TTAGATAAAG GAATTAAACC	2700
TTATTATCCA GAGCATGTAG TTAATCATTA CTTCCAGACG AGACATTATT TACATACTCT	2760

TTGGAAGGCC GGTATCTTAT ATAAAAGAGA GACAACACGT AGCGCCTCAT TTTGCGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCCCTCCAAA CCTCGACAAG	2880
GCATGGGGAC AAATCTTCC GTCCCCAATC CTCTGGGATT CTTTCCCAGT CACCAAGTTGG	2940
ACCCCTGCATT CAAAGCCAAC TCCGACAATC CCGATTGGGA CCTCAACCCA CACAAGGACA	3000
ACTGGCCGGA CTCCAACAAG GTGGGAGTGG GAGCATTGGG GCCGGGATTC ACTCCACCCC	3060
ATGGGGACT GTTGGGGTGG AGCCCTCAAG CTCAGGGCAT ACTCACAACT GTGCCAACAG	3120
CTCCTCCCTCC TGCCTCCACC AATCGGCAGT TAGGAAGGAA GCCTACTCCC CTGTCTCCAC	3180
CTCTAAGAGA CACTCATCCT CAGGCAATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 285:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 285:

AACTCCACCA CGTTCCACCA AACTCTCAA GATCCCAGAG TCAGGGCTCT GTACTTTCC	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGTTCAAG ACACGTCTC TTCCATATCG	120
TCAATCTTAT CGAAGACTGG GGACCCCTGTG CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGT ACAGGGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGAAC ACCCGTGTGT	300
CTTGGCCAAA ATTTCGAGTC CCAAATCTCC AGTCACTCAC CAACTGTTG TCCTCCGATT	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGGG CGTTTATCA TCTTCCTCTG CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGTG GGTTCTCTG GACTATCAAG GTATGTTGCC CGTTGTCCT	480
CTAAATTCCAG GATCATCAAC CACCAGCACC GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTACAAAAC CTACGGACGG AACTGCACC	600
TGTATTCCTCA TCCCCTCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCAAGT GGTTCTGAGG GCTTCCCCC	720
ACTGTCCTGGC TTTCAGTTAT ATGGATGATG TGGTTTGGG GGCCAAAGTCT GTACAACATC	780
TTGAGTCCT TTATGCCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTCAGAAAAC AAAAAGATGG GGCTACTCCC TCAACTTCAT GGGGTATGTA ATTGGAAGTT	900
GGGGCACCTT ACCCCAAGAA CATATTGTGT TGAAACTCAA ACAATGCTTT AGAAAACCTTC	960

CTGTAAACAG ACCTATTGAT TGGAAGGTGT GTCAACGAAT TGTGGGTCTT TTGGGATTTG	1020
CTGCTCCTT CACACAATGT GGTTATCCTG CTTTAATGCC TTTATATGCA TGTATACAAG	1080
CTAACACAGGC TTTTACTTT TCGCCAACGT ATAAGGCCTT TCTAACCAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GTCTGTGCCA AGTGTGGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGTCTCCTC	1260
TGCCGATCCA TACTGCGAA CTCCTAGCCG CTTGTTTGCT TCGCAGCAGG TCTGGAGCAA	1320
AACTTATCGG GACTGACAAT TCTGTTGTCC TTTCCCGCAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTTCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCCCGGG GCCGCTTGGG GCTCTACCGC CCGCTTCTCC	1500
GTCTGCCGTA CCGACCGACC ACGGGGCGCA CCTCTCTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCGTCT GCCGGACCGT GTGCACTTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CATCGGAACC TGCCCAAGGT CTTGCATAAG AGGACTCTG GACTTCAGC	1680
AATGTCACCG ACCGACCTTG AGGCATACTT CAAAGACTGT GTGTTTACTG AGTGGGAGGA	1740
GTTGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTTCCTTCT	1980
ATTCGAGATC TTCTCGACAC CGCCTCTGCT CTGTATCAGG AGGCCTTAAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAC GGCACTCAGG CAAGCTATTT TGTGTTGGGG TGAGTTGATG	2100
AATCTAGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCGGGA ATTAGTAGTC	2160
AGTTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGACAAAC TATTGTGGTT TCACATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAATATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACACCTC CTGCATATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCACC TCGCAGACGA	2400
AGGTCTCAAT CGCCCGGTG CAGAAGATCT CAATCTCCGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACGGG GCTTTATTCT TCTACGGTAC CTAGCTTAA	2520
TCCTAAATGG CAAACTCCTT CCTTCCCTGA CATTCAATTG CAGGAGGATA TCATTAATAG	2580
GTGTGAACAA TTTGTGGGAC CCCTCACAGT GAATGAAAAC AGGAGACTAA AATTGATTAT	2640
GCCTGCTAGG TTCTATCCC ATGTTACTAA ATATTTGCCC TTAGATAAAG GAATCAAACC	2700
TTATTATCCA GAGCATGTAG TTAATCATTA CTTCCAGACG AGACATTATT TACATACTCT	2760
TTGGAAGGCG GGTATCTTAT ATAAAAGAGA GACAACACGT AGCGCCTCAT TTTGCGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGAGGTTG GTCCCTCCAAA CCTCGACAAG	2880
GCATGGGGAC AAATCTTCC GTCCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940

ACCCCTGCATT CAAAGCCAAC TCCGACAATC CCGATTGGGA CCTCAACCCA CACAAGGACA	3000
ACTGGCCGGA CTCCAACAAG GTGGGAGTGG GAGCATTGG GCCTGGGATTC ACTCCACCCC	3060
ATGGGGGACT GTTGGGGTGG AGCCCTCAAG CTCAGGGCAT ACTCACAACT GTGCCAACAG	3120
CTCCTCCTCC TGCCCTCCACC AATCGGCAGT TAGGAAGGAA GCCTACTCCC CTGTCTCCAC	3180
CTCTAAGAGA CACTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 286:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 286:

AACTCCACCA CTTTCCACCA AACTCTCAA GATCCCAGAG TCAGGGCTCT GTACTTTCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAGC CCTGCTCAGA ATACTGTCTC AGCCATATCG	120
TCAATCTTAT CGAAGACTGG GGACCCCTGTG CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAAC ACCCGTGTGT	300
CTTGGCCAAA ATTGCAGTC CCAAATCTCC AGTCACTCAC CAACCTGTTG TCCTCCAATT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCC	480
CTAATTCCAG GATCATCAAC CACCAGCACG GGACCATGCA AGACCTGCAC AACTCCTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTACAAAAC CTATGGATGG AACTGCAAC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTCGTAGG GCTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATGCCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACCC	840
CTAACAAAAC AAAAAGATGG GGATATTCCC TTAACCTCAT GGGATATGTA ATTGGGAGTT	900
GGGGCACATG GCCACAGGAT CATATTGTAC AAAACTCAA ACTATGTTT AGAAAACCTC	960
CTGTAAACAG GCCTATTGAT TGGAAAGTTT GTCAACGAAT TGTGGTCTT TTGGGGTTG	1020
CTGCCCTTT TACGCAATGT GGATATCCTG CTTTAATGCC TTTATATGCA TGTATACAAG	1080
CAAAACAGGC TTTTACTTTT CCGCAACTT ACAAGGCCTT TCTCAGTAAA CAGTATATGA	1140

CCCTTTACCC CGTGCTCGG CAACGGCCTG GTCTGTGCCA AGTGTGGCT GACGCAACCC	1200
CCACTGGTTG GGGCTTGGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGTCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACCTCATCGG GACCGACAAT TCTGTCGTAC TCTCCCGCAA GTATAACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCAGGGACGTC CTTGTTTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCCTCCCGGG GCCGCTTGGG GCTCTACCGC CCGCTTCTCC	1500
GTCTGCCGTA CGTCCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACCTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCGGAACC TGCCCAAGGT CTTGCATAAG AGGACTCTTG GACTTTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT GTGTTAACG AGTGGGAGGA	1740
GCTGGGGAG GAGATTAGGT TAAAGGTCTT TGTACTCGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAG TCATCTCTTG TTCATGTCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCCTAT	1920
AAAGAATTG GAGCTACTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTCCGTCG	1980
GTGCGGGACC TCCTAGATAC CGTCTCTGCT CTGTATCGGG AAGCCTTAAA ATCTCCTGAG	2040
CATTGCTCAC CTCACCACAC AGCACTCAGG CAAGCTATTG TGTGCTGGGG GGAATTAATG	2100
ACTCTAGCTA CCTGGGTGGG TAATAATTG GAAGATCCAG CATCCCGGGA TCTAGTAGTC	2160
AATTATGTTA ACACAAACAT GGGCTTAAAG ATCAGGCAAC TATGGTGGTT TCACATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTG GAATATTGG TATCTTTGG AGTGTGGATT	2280
CGCACCTCTC CTGCCTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CACCGCGTCG CAGAAGATCT CAATCTCGGG AATCCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGAA ACTTACGGG GCTTTATTCT TCTACAGTAC CTGTCTTAA	2520
TCCTGAATGG CAAACTCCTT CTTTCCAGA CATTCAATTAA CAGGAGGACA TTGTTGATAG	2580
ATGTAAGCAA TTTGTGGAC CCCTTACAGT AAATGAAAAC AGGAGACTAA AATTAATAAT	2640
GCCTGCTAGA TTTTATCCA ATGTTACCAA ATATTTGCCCT TAGATAAAG GTATCAAACC	2700
TTATTATCCA GAGCATGTAG TTAATCATTA CTTCCAGACT AGACATTATT TGCATACTCT	2760
TTGGAAGGCG GGTATCTTAT ATAAAAGAGA GTCAACACAT AGCCCTCAT TTTGCGGGTC	2820
ACCTTATTCT TGGGAACAAG ATCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGAAAAG	2880
GCATGGGAC AAATCTTCT GTCCCCAATC CCCTGGGATT CTTCCCCGAT CATCAGTTGG	2940
ACCTGCATT CAAAGCCAAC TCAGAAAATC CAGATTGGGA CCTCAACCCA CACAAGGACA	3000
ACTGCCCGGA CGCCACAAAG GTGGGAGTGG GAGCATTGGC GCCAGGATTC ACCCCCTCCCC	3060
ATGGGGACT GTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ACTCACATCT GTGCCAGCAG	3120

CTCCTCCTCC TGCCTCCACC AATCGGCAGT CAGGACGGCA GCCTACTCCC CTATCTCCAC	3180
CTCTAAGGGA CACTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 287:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: DNA (genomic)

- (iii) HYPOTHETICAL: NO

- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 287:

AACTCCACCA CTTTCCACCA AACTCTTCAA GATCCCAGG TCAGGGCCCT GTACTTCCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTGAGC CCTGCTCAGA ATACTGTCTC TGCCATATCG	120
TCAATCTTAT CGAACAGCTGG GGACCCCTGTA CCGAACATGG AGAACATCGC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGT ACAGGGCGGGG TTTTTCTTGT TGACAAAAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGAAC ACCCGTGTGT	300
CTTGGCCAAA ATTTCAGAGTC CCAAATCTCC AGTCACTCAC CAACCTGTTG TCCTCCAATT	360
TGTCCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTG CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTG GGTTCTCTG GACTATCAAG GTATGTTGCC CGTTTGTCC	480
CTAATTCCAG GATCATCAAC AACCAAGCACC GGACCATGCA AAACCTGCAC AACTCCTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTACAAAAC CTACGGATGG AAACTGCACC	600
TGTATTCCA TCCCCATCATC TTGGGCTTTC GCAAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCTT GGCTCAGTTT ACTAGTGCCA TTTGTTCAAGT GGTCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATA TGGTTTGGG GGCCAAAGTCT GTACAACATC	780
TTGAGTCCCT TTATGCCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTCACAAAAC AAAAAGATGG GGATATTCCC TTAACCTCAT GGGATATGTA ATTGGGAGCT	900
GGGGCACATT GCCACAGGAA CATATTGTAC AAAAATCAA AATGTGGTTT AGGAAACTTC	960
CTGTAAACAG GCCTATTGAT TGGAAAGTAT GTCAACGAAT TGTGGTCTT TTGGGTTTG	1020
CCGCCCTTT CACGCAATGT GGATATCCTG CTTTAATGCC TTTATATGCA TGTATACAAG	1080
CAAAACAGGC TTTTACTTTC TCGCCAACCT ACAAGGCCTT TCTAACTAAA CAGTATCTGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GTCTGTGCCA AGTGTGGCT GACGCAACCC	1200
CCACTGGTTG GGGCTTGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGTCTCCTC	1260

TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTGC TCGCAGCCGG TCTGGGGCAA	1320
AACTCATCGG GACTGACAAT TCTGCGTGC TCTCCCGCAA GTATACATCA TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC CGGGGACGTC CTTGTTTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCTTCCCGGG GCCGCTTGGG GCTCTACCGC CCGCTTCTCC	1500
GCCTGTTGTA CCGACCGACC ACGGGGCGCA CCTCTCTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCCTG GTGCACCTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACGGGAACC TGCCCAAGGT CTTGCATAAG AGGACTCTTG GACTTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT GTGTTAATG AGTGGGAGGA	1740
GTTGGGGAG GAGGTTAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
GTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTCCGTCG	1980
GTGCGAGATC TCCTCGACAC CGCCTCTGCT TTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAAC GGCACTCAGG CAAGCTATTG TGTGTTGGG TGAGTTAATG	2100
AATCTAGCCA CCTGGGTGGG AAGTAATTG GAAGATCCGG CATCCAGGGA ATTAGTAGTC	2160
AGCTATGTCA ACGTTAATAT GGGCCTAAAA ATCAGACAAC TATTGTTGGTT TCACATTCC	2220
TGTCTTACTT TTGGGAGAGA AACTGTTCTT GAATATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CTGCATATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGAAGAGG CAGGTCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACACAT AAGGTGGAA ACTTACCGG GCTTTATTCT TCTACGGTAC CTTGCTTAA	2520
TCCTAAATGG CAAACTCCTT CTTTCCTGA CATTCAATTG CAGGAGGACA TTGTTGATAG	2580
ATGTAAGCAA TTTGTGGGC CCCTTACAGT AAATGAAAAC AGGAGACTAA AATTAATTAT	2640
GCCCCCTAGG TTTTATCCA ATGTTACTAA ATATTGCCC TTAGATAAAG GGATCAAACC	2700
GTATTATCCA GAGTATGTAG TTAATCATTA CTTCCAGACG CGACATTATT TACACACTCT	2760
TTGGAAGGCG GGGATCTTAT ATAAAAGAGA GTCCACACGT AGCGCCTCAT TTTGCGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGAAAAG	2880
GCATGGGGAC AAATCTTCT GTCCCCAATC CTCTGGGATT CTTCCCCGAT CATCAGTTGG	2940
ACCTGCATT CAAAGCCAAC TCAGAAAATC CAGATTGGG CCTCAACCCG AACAGGACA	3000
ACTGGCCCGA CGCCAACAAG GTGGGAGTGG GAGCATTGG GCCAGGGTTC ACCCCTCCCC	3060
ATGGGGACT GTTGGGGTGG AGCCCTCAGG CTCAGGGCCT ACTCACAACG GTGCCAGCAG	3120
CTCCTCCTCC TGCCTCCACC AATCGGCAGT CAGGAAGGCA GCCTACTCCC TTATCCCCAC	3180
CTCTAAGGGA CACTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 288:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3213 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 288:

AACTCCACCA CATTTCACCA AGTCCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCC	60
CCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTGCGA CTACTGCCTC ACCCATATCG	120
TCAATCTCCT CGAGGACTGG GGACCCCTGCA CCGAACATGG AGAGCACAAAC ATCAGGATT	180
CTAGGACCCC TGCTCGTGT ACAGGCCGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TATTCCCTTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGT GGTTCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCT	480
CTACTTCCAG GAACATCAAC CACCAGCACG GGACCATGCA AGACCTGCAC GATTCCCTGCT	540
CAAGGAACCT CTATGTTCC CTCTTGTGC TGTACAAAAC CTTGGACGG AAACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGGG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTCGTAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACTTCAT GGGATATGTA ATTGGCAGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTT CGGAAACTGC	960
CTGTAAATAG ACCTATTGAC TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTAATGCC TTTATATGCA TGTATACAAT	1080
CTAACAGGGC TTTCACCTTC TCGCCAACCT ACAAGGCCCT TCTGTTAAA CAATATCTGC	1140
ACCTTTACCC CGTTGCCCGG CGAACGGCTC TCTGCCAAGT ATTTGCTGAC GCAACCCCCA	1200
CTGGATGGGG CTTGGCCATA GGCCATCGGC GCATGCGTGG AACCTTGTG GCTCCTCTGC	1260
CGATCCATAC TCGGAAACTC CTAGCAGCTT GTTTGCTCG CAGCCGGTCT GGAGCGAAAC	1320
TCATCGGGAC TGACAACCTCG GTTGTCTCT CTCGGAAATA CACCTCATTC CCATGGCTGC	1380
TCGGGTGTGC TGCCAACTGG ATCCTGCGCG GGACGTACTT TGTTTACGTC CCGTCGGCGC	1440
TGAATCCCGC GGACGACCCCG TCTCGCGGCC GTTTGGGCCT CATCGTCCC CTTCTTCATC	1500

TGCGGGTCCG	GCCGACCACG	GGCGCACCT	CTCTTACGC	GGTCTCCCCG	TCTGTGCCTT	1560
CTCATCTGCC	GGACCGTGTG	CACTTCGCTT	CACCTCTGCA	CGTCGCATGG	AGACCACCGT	1620
GAACGCCGAT	CAGGTCTTGC	CCAAGGTCTT	ACATAAGAGG	ACTCTGGAC	TCTCAGCAAT	1680
GTCAACGTCC	GACCTTGAGG	CATACTCAA	AGACTGCTTG	TTTAAAGACT	GGGAGGACTT	1740
GGGGGAGGAG	ATTAGGTTAA	TGATCTTGT	ACTAGGAGGC	TGTAGGCATA	AATTGGTCTG	1800
TTCACCAGCA	CCATGCACT	TTTTCACCT	CTGCCTAATC	ATCTCATGTT	CATGTCCTAC	1860
TGTTCACGCC	TCCAAGCTGT	GCCTTGGGTG	GCTTTGGGGC	ATGGACATTG	ACCCGTATAA	1920
AGAATTGGA	GCTTCTGTGG	AGTTACTCTC	TTTTTGCCCT	TCTGATTCT	TTCCTTCCAT	1980
TCGAGATCTC	CTCGACACCG	CCTCTGCTCT	GTATAGGGAG	GCCTTAGAGT	CTCCGGAACA	2040
TTGTTCACCT	CATCATACAG	CACTCAGGCA	AGCTATTCTG	TGTTGGGTG	AGTTGATGAA	2100
TCTGGCCACC	TGGGTGGGAA	GTAATTGGA	AGACCCAGCA	TCCAGGAAAC	TAGTAGTCAG	2160
CTATGTCAAT	GTTAATATGG	GCCTAAAAT	CAGACAACTA	TTGTGGTTTC	ACATTTCTG	2220
CCTTACTTT	GGAAGAGAAA	CTGTTTGGGA	GTATTTGGTA	TCTTTGGAG	TGTGGATTCTG	2280
CACTCCTCCC	GCTTACAGAC	CACCAATGC	CCCTATCTTA	TCAACACTTC	CGGAAACTAC	2340
TGTTGTTAGA	CGACGAGGCA	GGTCCCTAG	AAGAAGAACT	CCCTCGCCTC	GCAGACGAAG	2400
ATCTGAATCG	CCCGTGCAGCA	GAAGATCTCA	ATCTCGGGAA	TCTCAATGTT	AGTATCCCTT	2460
GGACTCATAA	GGTGGGAAAC	TTTACTGGGC	TTTATTCTTC	TACTGTACCT	GTCTTTAAC	2520
CTGAGTGGCA	AACTCCCTCC	TTTCCTCACA	TTCATTTACA	GGAGGACATT	ATTAATAGAT	2580
GTCAACAATA	TGTGGGCCCT	CTTACAGTTA	ATGAAAAAAG	GAGATTAAAA	TTAATTATGC	2640
CTGCTAGGTT	TTATCCTAAA	CTTACCAAAT	ATTTGCCCTT	GGATAAAGGC	ATTAACCTT	2700
ATTATCCTGA	ACATGCAGTT	AATCATTACT	TCAAAACTAG	GCATTATTTA	CATACTCTGT	2760
GGAAGGCGGG	CATTCTATAT	AAGAGAGAAA	CTACACGCAG	CGCCTCATTT	TGTGGGTAC	2820
CATATTCTTG	GGAACAAGAG	CTACAGCATG	GGAGGTTGGT	CTTCCAAACC	TCGACAAGGC	2880
ATGGGGACGA	ATCTTCTGT	TCCCATTCC	CTGGGATTCT	TTCCCGATCA	CCAGTTGGAC	2940
CCTGCGTTCG	GAGCCAAC	AAACAATCCA	GATTGGACT	TCAACCCAA	CAAGGATCGT	3000
TGGCCAGAGG	CAAATCAGGT	AGGAGCGGG	GCATTGGGC	CAGGGTACCC	CCCACCACAC	3060
GGCGGTCTT	TGGGGTGGAG	CCCTCAGGCT	CAGGGCATAT	TGACAACCGT	GCCAGCAGCA	3120
CCTCCTCCTG	CCTCCACCAA	TCGGCAGTCA	GGAAGACAGC	CTACTCCCAT	CTCTCCACCT	3180
CTAAGAGACA	GTCATCCTCA	GGCCATGCAG	TGG			3213

(2) INFORMATION FOR SEQ ID NO: 289:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3213 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 289:

AACTCCACCA CATTTCACCA AGTCCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCCCT	60
CCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTCCT CGAGGACTGG GGACCCTGCA CCGAACATGG AGAGCACAAAC ATCAGGATT	180
CTAGGACCCC TGCTCGTGT ACAGGGGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTCGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGTG GTTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCC	480
CTACTTCCAG GAACATCAAC CACCAGCACG GGACCATGCA AGACCTGCAC GATTCCGTGCT	540
CAAGGAACCT CTATGTTCC CTCTTGTG TGACAAAAC CTTCGGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGGG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTT ACTAGTGCCA TTTGTTCACT GGTTCTGAGG GCTTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACTTCAT GGGATATGTA ATTGGCAGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTT CGGAAACTGC	960
CTGTAAATAG ACCTATTGAC TGGAAAGTAT GTCAAAGAAT TGTGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTAATGCC TTTATATGCA TGTATACAAT	1080
CTAACGAGGC TTTCACTTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATATCTGC	1140
ACCTTACCC CGTTGCCCGG CGAACGGCTC TCTGCCAAGT ATTTGCTGAC GCAACCCCCA	1200
CTGGATGGGG CTTGGCCATA GGCCATCGGC GCATGCGTGG AACCTTGTG GCTCCTCTGC	1260
CGATCCATAC TGCGGAACTC CTAGCAGCTT GTTTGCTCG CAGCCGGTCT GGAGCGAAAC	1320
TCATCGGGAC TGACAACTCG GTTGTCTCT CTCGGAAATA CACCTCATTC CCATGGCTGC	1380
TCGGGTGTGC TGCCAACTGG ATCCTGCGCG GGACGTACTT TGTTACGTC CCGTCGGCGC	1440
TGAATCCCGC GGACGACCCG TCTCGCGGCC GTTTGGGCCT CATCCGTCCC CTTCTTCATC	1500
TGCGGTTCCG GCCGACCACG GGGCGCACCT CTCTTACGC GGTCTCCCCG TCTGTGCCTT	1560
CTCATCTGCC GGACCGTGTG CACTTCGCTT CACCTCTGCA CGTCGCATGG AGACCACCGT	1620
GAACGCCGAT CAGGTCTTGC CCAAGGTCTT ACATAAGAGG ACTCTGGAC TCTCAGCAAT	1680

GTCAACGTCC GACCTTGAGG CATACTCAA AGACTGCTT TTTAAAGACT GGGAGGACTT	1740
GGGGGAGGAG ATTAGGTTAA TGATCTTGT ACTAGGAGGC TGTAGGCATA AATTGGTCTG	1800
TTCACCAGCA CCATGCAACT TTTTCACCT CTGCCTAATC ATCTCATGTT CATGTCCTAC	1860
TGTTCACGCC TCCAAGCTGT GCCTTGGGTG GCTTTGGGC ATGGACATTG ACCCGTATAA	1920
AGAATTGGA GCTTCTGTGG AGTTACTCTC TTTTTGCCT TCTGATTCT TTCCCTCCAT	1980
TCGAGATCTC CTCGACACCG CCTCTGCTCT GTATAGGGAG GCCTTAGAGT CTCCGGAACA	2040
TTGTTCACCT CATCATAACAG CACTCAGGCA AGCTATTCTG TGTTGGGTG AGTTGATGAA	2100
TCTGGCCACC TGGGTGGAA GTAATTGGA AGACCCAGCA TCCAGGGAAC TAGTAGTCAG	2160
CTATGTCAAT GTTAATATGG GCCTAAAAAT CAGACAACTA TTGTGGTTTC ACATTTCTG	2220
CCTTACTTTT GGAAGAGAAA CTGTTTGGGA GTATTGGTA TCTTTGGAG TGTGGATTG	2280
CACTCCTCCC GCTTACAGAC CACCAAATGC CCCTATCTTA TCAACACTTC CGGAAACTAC	2340
TGTTGTTAGA CGACGAGGCA GGTCCCTAG AAGAAGAACT CCCTCGCCTC GCAGACGAAG	2400
ATCTGAATCG CCGCGTCGCA GAAGATCTCA ATCTCGGGAA TCTCAATGTT AGTATCCCTT	2460
GGACTCATAA GGTGGAAAC TTTACTGGGC TTTATTCTTC TACTGTACCT GTCTTTAAC	2520
CTGAGTGGCA AACTCCCTCC TTTCCCTACA TTCATTTACA GGAGGACATT ATTAATAGAT	2580
GTCAACAATA TGTGGGCCCT CTTACAGTTA ATGAAAAAAG GAGATTTAA TTAATTATGC	2640
CTGCTAGGTT TTATCCTAAA CTTACCAAAT ATTTGCCCTT GGATAAAGGC ATTAACCTT	2700
ATTATCCTGA ACATGCAGTT ATCATTACT TCAAAACTAG GCATTATTAA CATACTCTGT	2760
GGAAGGCAGGG CATTCTATAT AAGAGAGAAA CTACACGCAG CGCCTCATTT TGTGGGTCA	2820
CATATTCTTG GGAACAAGAG CTACAGCATG GGAGGTTGGT CTTCCAAACC TCGACAAAGGC	2880
ATGGGGACGA ATCTTTCTGT TCCCAATCCT CTGGGATTCT TTCCCGATCA CCAGTTGGAC	2940
CCTGCCTTCG GAGCCAACTC AAACAAATCCA GATTGGACT TCAACCCCAA CAAGGATCGT	3000
TGGCCAGAGG CAAATCAGGT AGGAGCGGGA GCATTCGGGC CAGGGTACCC CCCACCACAC	3060
GGCGGTCTTT TGGGGTGGAG CCCTCAGGCT CAGGGCATAT TGACAACCGT GCCAGCAGCA	3120
CCTCCCTCTG CCTCCACCAA TCGGCAGTCA GGAAGACAGC CTACTCCCAT CTCTCCACCT	3180
CTAAGAGACA GTCATCCTCA GGCCATGCAG TGG	3213

(2) INFORMATION FOR SEQ ID NO: 290:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 290:

AACTCCACAA	CATTCCACCA	AGCTCTGCTA	GATCCCAGAG	TGAGGGGCCT	ATATTTCCCT	60
GCTGGTGGCT	CCAGTTCCGG	AACAGTAAAC	CCTGTTCCGA	CTACTGTCTC	ACCCATATCG	120
TCAATCTTCT	CGAGGACTGG	GGACCCCTGCA	CCGAACATGG	AGAGCACAAAC	ATCAGGATTC	180
CTAGGACCCC	TGCTCGTGT	ACAGGCCGGG	TTTTCTTGT	TGACAAGAAC	CCTCACAATA	240
CCACAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGGAGC	ACCCACGTGT	300
CCTGGCCAAA	ATTCGCAGTC	CCCAACCTCC	AATCACTCAC	CAACCTCTG	TCCTCCAATT	360
TGTCCCTGGTT	ATCGCTGGAT	GTGTCTGCGG	CGTTTTATCA	TATCCCTCTT	CATCCTGCTG	420
CTATGCCTCA	TCTTCTTGT	GGTTCTTCTG	GACTACCAAG	GTATGTTGCC	CGTTTGTCCCT	480
CTACTTCCAG	GAACATCAAC	TACCAGCACG	GGACCATGCA	AGACCTGCAC	GATTCCCTGCT	540
CAAGGAACCT	CTATGTTCC	CTCTTGTGC	TGTACAAAAC	CTTCGGACGG	AAACTGCAC	600
TGTATTCCCA	TCCCCATCATC	CTGGGCTTTC	GCAAGATTCC	TATGGGAGTG	GGCCTCAGTC	660
CGTTCTCCT	GGCTCAGTTT	ACTAGTGC	TTTGTTCAGT	GGTTCCGAGG	GCTTTCCCCC	720
ACTGTTGGC	TTTCAGTTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAACATC	780
TTGAGTCCCT	TTTACCTCT	ATTACCAATT	TTCTTTGTC	TTTGGGTATA	CATTTGAACC	840
CTAATAAAAC	CAAACGTTGG	GGCTACTCCC	TTAACCTCAT	GGGATATGTA	ATTGGAAGTT	900
GGGGTACTTT	ACACAGGAA	CATATTGTAT	AAAAACTCAA	GCAATGTTT	CGAAAAC	960
CTGTAAATAG	ACCTATTGAT	TGGAAAGTAT	GTCAAAGAAT	TGTGGTCTT	TTGGGCTTTG	1020
CTGCCCTTT	TACACAATGT	GGCTATCCTG	CCTTGATGCC	TTTGTATGCA	TGTATAACAAT	1080
CTAACGCAGGC	TTTCACCTTC	TCGCCAACTT	ATAAGGCCTT	TCTGTGTCAA	CAATAACCTGC	1140
ACCTTTACCC	CGTTGCCCGG	CAACGGTCAG	GTCTCTGCCA	AGTGTTCGCT	GACGCAACCC	1200
CCACTCGATG	GGGCTTGGCC	ATAGGCCATC	GGCGCATGCG	TGGAACCTTT	GTGGTTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCAG	CTTGTTCAG	TCGCGACCGG	TCTGGAGCAA	1320
AACTTATCGG	GACTGACAAAC	TCGGTTGTCC	TCTCTCGGAA	ATACACCTCC	TTCCCATGGC	1380
TGCTCGGGTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTGTCCTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCGTCTCGGG	GCCGTTGGG	CCTCTACCGT	CCCTTGCTTT	1500
CTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTAA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACCTCG	CTTCACCTCT	GCACGTGCA	TGGAGACCAC	1620
CGTGAACGGC	CACCAGGTCT	TGCCCAAGCT	CTTACATAAG	AGGACTCTTG	GACTCTCAGC	1680
AATGTCAACA	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTAAAG	ACTGGGAGGA	1740
GTTGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAAATTGGT	1800
CTGTTCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCAA	TCATCTCATG	TTCATGTCCT	1860

ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGCG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTTCCTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAAC AGCACTCAGG CAAGCTATTG TGTGTTGGGG TGAGTTGATG	2100
AATTTGGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGGAA ATTAGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCCTAAAAA ATCAGACAAAC TATTGTTGG TTCAATTTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTG TGTCCTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCCTTAA	2520
TCCTGAGTCC CAAACTCCCT CCTTTCTAA CATTCAATTAA CAGGAGGACA TTATTAATAG	2580
ATGTCACAA TATGTGGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCC TTGGATAAAG GCATTAACCC	2700
TTATTATCCT GAACATGCAG TTAATCATTA CTTCAAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAAAGAGA AACTACACGC AGCGCTTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACGGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGAC GAATCTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAAGTTGG	2940
ACCCCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAAGGATC	3000
ACTGCCAGA GGCAATCAAG GTAGGAGCGG GAGACTTCGG GCCAGGGTTC ACCCCACAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGCAG	3120
CCGCTCTCC TGTTCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCRTGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 291:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 291:

AACTCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG TCAATCTTCT CGAGGACTGG GGACCCGTCA CGAACATGG AGAGCACAAAC ATCAGGATTC	120 180
CTAGGACCCC TGCTCGTGT ACAGGGGGG TTTTCTTGT TGACAAGAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTG TCCTCCAATT	360
TGTCTGGCT ATCGCTGGAT GTGTCTGCG CGTTTTATCA TATTCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTCTG GACTACCAAG GTATGTTGCC CGTTTGTCCCT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTCC CTCTTGTGG TGTACAAAAC CTTGGACGG AAAACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTCGCAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TAAACTTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAT TAAAACCTCAA GCAATGTTT CGGAAACTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATAAACAT	1080
CTAACGAGC TTTCACTTTC TCGCCAACCTT ATAGGCCCTT TCTGTGTCAA CAATACCTGC	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGGT GACGCAACCC	1200
CCACTGGATG GGGCTTGCC ATAGGCCATC GGCGCATGCG TGGAACCTTT GTGGCTCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AACTTATCGG GACTGACAAC TCTGTTGTCC TCTCTCGAA ATACACCTCC TTCCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC CGGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG CCTCTACCGT CCCCTCTTC	1500
ATCTGCCGTT CCAGCCGACC ACGGGGCGCA CCTCTCTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTCACCTCT GCACGTGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCTAAGCT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTAAAG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCAA TCATCTCATG TTCATGTCTC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTCTGT GGAGTTACTC TCTTTTTGTC CTTCTGACTT CTTTCCTTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040

CATTGTCAC CTCACCATAAC AGCACTCAGG CAAGCTATCC TGTGTTGGGG TGAGTTGATG	2100
AATTGGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGGA ATTAGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCTAAAA ATCAGACAAC TATTGTGGTT TCACATTC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTAA	2520
TCCTGAGTGC CAAACTCCCT CCTTCCTAA CATTCAATTAA CAAGAGGATA TTATTAATAG	2580
ATGTCAACAA TATGTGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA ATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCCCT TTGGATAAAG GCATTAACC	2700
TTATTATCCT GAACATGCAG TTAATCATTAA CTTCAAAACT AGGCATTATT TACATACGCT	2760
GTGGAAGGCT GCCATTCTAT ATAAAAGAGA AACTACACGC AGCGCTTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGAC GAATCTTCT GTTCCAATC CTCTGGGATT CTTTCCGAT CACCAGTTGG	2940
ACCCCTGCGTT CGGAGCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAAGGATC	3000
ACTGGCCAGA CGGAATCAAG GTAGGAGCGG GAGACTTCGG GCCAGGGTTC ACCCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCTCAGG CTCAGGGCAT CTTGACAACA GTGCCAGCAG	3120
CTCCTCCTCC TGCCTCCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAACAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 292:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 292:

AACTCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCCTGCA CCGAACATGG AGAGCACAAAC ATCAGGATTC	180

CTAGGACCCC TGCTCGTGT ACAGGCAGGG TTTTCTTGT TGACAAGAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTG TCCTCCA ACT	360
TGTCTGGCT ATCGCTGGAT GTGCTGCGG CGTTTATCA TATTCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGT GGTTCTTCTG GACTACCAAG GTATGTTGCC CGTTGTCCT	480
CTACTTCCAG GAACATCAAC TACCAGCAGG GGACCATGCA GAACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTCC CTCTGTTGC TGTACAAAAC CTTGGACGG AAAACTGCACT	600
TGTATTCCCA TCCCACATC CTGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCA GTGCTGAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGCTAT ATGGATGATG TGGTATTGGG GGCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAAGTT	900
GGGGTACTTT ACCGCAGGAA CATATTGTAC AAAAATCAA GCAATGTTT CGAAAATTGC	960
CTGTAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAACGCAGGC TTTCACCTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATATCTAA	1140
ACCTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACGGGTTG GGGCTTGGCC ATAGGCCATC GGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTGC TCGCAGCCGG TCTGGAGCGA	1320
AACTTATCGG AACCGACAAAC TCAGTTGTCC TCTCTCGAA ATACACCTCC TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC CGGGGACGTC CTTGTCTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG CCTCTACCGT CCCCTTCTTC	1500
ATCTGCCGTT CGGGCCGACC ACGGGGCGCA CCTCTCTTA CGCGGTCTCC CCGTCTGTC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTCACCTCT GCACGTAGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACACAAG AGGACTCTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAAG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCCC CTCTGCCAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTTCCTCT	1980
ATT CGAGATC TCCTCGACAC CGCCTCTGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAAC AGCACTCAGG CAAGCTATTC TGTGTTGGGG TGAGTTGATG	2100
AATCTGGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGGAA ATTAGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCCTAAAA ATTAGACAAC TATTGTGGTT TCACATTCC	2220

TGCCTTACTT TTGGAAGAGA AACTGTCCTT GAGTATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTAA	2520
TCCTGATTGG AAAACTCCCT CCTTCCTCA CATTCAATTAA CAGGAGGACA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTGACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCC TTGGACAAAG GCATTAACC	2700
GTATTATCCT GAATATGCAG TTAATCATTAA CTTCAAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAGAGAGA AACTACACGC AGCGCCTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTCT GTTCCAATC CTCTGGGATT CTTCCCGAT CACCAGTTGG	2940
ACCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCCC AACAAAGGATC	3000
ACTGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTGG TCCAGGGTTC ACCCCACCC	3060
ACGGAGGCCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA CTGCCAGCAG	3120
CACCTCCTCC TGCCTCCACC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 293:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3188 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 293:

AATTCCACAA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCCTGCA CCGAACATGG AGAACACAAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGCAGGG TTTTTCTTGT TGACAAGAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTGCGACTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360

TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TATTCCCTTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTG GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTGTCCT	480
CTACTTCCAG GAACATCAAC CACCAGCACG GGGCCATGCA AGACCTGCAC GATTCCCTGCT	540
CAAGGAACCT CTATGTTCC CTCTTGTG TGTAACAAAC CTTCGGACGG AACTGCACT	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCCTAGTC	660
CGTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GTTCTCGTAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTAATAAAAC CAAACGTTGG GGCTACTCCC TAAACTTCAT GGATATGTA ATTGGAAAGTT	900
GGGGTACTTT ACCGCAGGAA CATATTGTAC TAAACTCAA GCAATGTTT CGAAAATTGC	960
CTGTAAATAG CCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGTCTT TTGGGCTTG	1020
CTGCCCTTT TACACAATGC GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAACGCAGGC TTTCACTTTC TCGCCAACCT ATAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGCT GACGCCAACCC	1200
CCACTGGATG GGGCTTGGCC ATAGGCCATC GGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTG TGCGAGCCGG TCTGGAGCGA	1320
AACTTATCGG AACCGACAAC TCTGTTGTCC TCTCTCGAA ATACACCTCC TTTCCATGGC	1380
TGCTAGGGTG TGCTGCCAAC TGGATCCTGC CGGGGACGTC CTTTGTCTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG GCTCTACCGT CCCCTTCTTC	1500
TTCTGCCGTT CGGGCCGACC ACGGGGCGCA CCTCTCTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCGGGACCGT GTGCACTTCG CTTCACCTCT GCACGTGCA TGGAGACAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
CATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT GTGTTAAAG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAACCTTTT	1800
CACCTCTGCC TAATCATCTC ATGTTCATGT CCTACTGTTC AAGCCTCCAA GCTGTGCCCT	1860
GGGTGGCTTT GGGGCATGGA CATTGACCCG TATAAAGAAT TTGGAGCATC TGTGGAGTTA	1920
CTCTCTTTT TGCCTCTGA CTTCTTCCG TCTATTGAG ATCTCCTTGA CACCGCCCT	1980
GCTCTGTATC GGGAGGCCTT AGAGTCTCCG GAACATTGTT CACCTCACCA TACAGCACTC	2040
AGGCAAGCTA TTCTGTGTTG GGGTGACTTA ATGAATCTGG CCACCTGGGT GGGAGTAAT	2100
TTGGAAGACC CAGCATCCAG GGAATTAGTA GTCAGCTATG TCAATGTTAA TATGGCCTA	2160
AAAATCAGAC AACTATTGTG GTTTCACATT TCCTGCCTTA CTTTGGAAAG AGAAACTGTT	2220
TTGGAGTATT TGGTATCTTT TGGAGTGTGG ATTGCACTC CTCCCGCTTA CAGACCACCA	2280
AATGCCCTA TCTTATCAAC ACTTCCGGAA ACTACTGTTG TTAGACGACG AGGCAGGTCC	2340
CCTAGAAGAA GAACTCCCTC GCCTCGCAGA CGAAGGTCTC AATGCCCGCG TCGCAGAAGA	2400

TCTCAATCTC GGGAACTCTCA ATGTTAGTAT CCCTTGACT CATAAGGTGG GAAACTTTAC	2460
TGGGCTTAT TCTTCTACTG TACCTGTCTT TAATCCCGAG TGGCAAACTC CCTCCTTCC	2520
TCACATTCAAT TTACAGGAGG ACATTATTAA TAGATGTCAA CAATATGTGG GCCCTCTTAC	2580
GGTTAATGAA AAAAGGAGAT TAAAATTAAT TATGCCTGCT AGGTTCTATC CTAACCTTAC	2640
TAAATATTTG CCCTTAGACA AAGGCATTAA ACCGTATTAT CCTGAACATG CAGTTAATCA	2700
TTACTTCAAA ACTAGGCATT ATTTACATAC TCTGTGGAAG GCTGGCATTC TATATAAGAG	2760
AGAAAATACA CGCAGCGCCT CATTGGTGG GTCACCATAAT TCTTGGGAAC AAGAGCTACA	2820
GCATGGGAGG TTGGTCTTCC AACACCTCGAC AAGGCATGGG GACGAATCTT TCTGTTCCA	2880
ATCCTCTGGG ATTCTTCCC GATCACCAGT TGGACCCCTGC GTTCGGAGCC AACTCAAACA	2940
ATCCAGATTG GGACTTCAAC CCCAACAAAGG ATCAATGGCC AGAGGCAAAT CAGGTAGGAG	3000
CGGGAGCATT CGGGCCAGGG TTCACCCAC CACACGGCGG TCTTTGGGG TGGAGCCCTC	3060
AGGCTCAGGG CATATTGACA ACAGTGCCAG CAGCACCTCC TCCTGCCTCC ACCAATCGGC	3120
AGTCAGGAAG ACAGCCTACT CCCATCTCTC CACCTCTAAG AGACAGTCAT CCTCAGGCCA	3180
TGCAGTGG	3188

(2) INFORMATION FOR SEQ ID NO: 294:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3214 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 294:

AACTCCACAA CATTCCACCA AGCTCTGCTA GACCCCAGAG TGAGGGGCCT ATACTTCCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTCCT CGAGGACTGG GGACCCGTGCA CCGAACATGG AGAACACAAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGGGGGG TTTTCTTGT TGACAAGAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTGTT GGTTCTCTG GACTACCAAG GTATGTTGCC CGTTTGTGCT	480
CTACTTCCAG GAACATCAAC TACCAAGCAGG GGACCATGCA AGACCTGCAC GATTCCGT	540

CAAGGAACCT CTATGTTCC CTCTGTTGC TGTACAAAAC CTTCGGACGG AACTGCAC	600
TGTATTCCA TCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGGG GGCTCAGTC	660
CGTTCTCCT GGCTCAGTT ACTAGTGCCA TTTGTTCACT GGTCGTAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTAATAAAAC CAACGTTGG GGCTACTCCC TTAACTTCAT GGGATATGTA ATTGGATGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTT CGAAAATGCGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAGAGACT TGTGGGTCTT TTGGGCTTTG	960 1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTAATGCC TTTATATGCA TGTATACAAT	1080
CTAACGCAGGC TTTCACTTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCT ATCGGCCATA GCCGCATGCG CGGACCTTG TGGCTCCTCT	1260
GCCGATCCAT ACTGCGGAAC TCCTAGCAGC TTGTTTGCT CGCAGGCGGT CTGGAGCGAA	1320
ACTTATCGGC ACCGACAACCT CTGTTGTCCT CTCTCGAAA TACACCTCCT TTCCATGGCT	1380
GCTAGGGTGT GCTGCCAACT GGATCCTGCG CGGGACGTCC TTTGTCTACG TCCCGTCGGC	1440
GCTGAATCCC GCGGACGACC CGTCTGGGG CCGTTGGGA CTCTACCGTC CCCTCTTCA	1500
TCTGCCGTTG CGGCCGACCA CGGGCGCAC CTCTCTTAC GCGGTCTTT TGTCTGTGCC	1560
TTCTCATCTG CCGGTCCGTG TGCACTTCGC TTCACCTCTG CACGTGCGAT GGAGACCACC	1620
GTGAACGCC ACCAGGTCTT GCCCAAGGTC TTACATAAGA GGACTCTTGG ACTCTCAGCG	1680
ATGTCAACGA CCGACCTTGA GGCATACCTTC AAAGACTGTT TGTTAAGGA CTGGGAGGAG	1740
TTGGGGGAGG AGATTAGGTT AAAGGTCTTT GTACTAGGAG GCTGTAGGCA TAAATTGGTC	1800
TGTTCACCAAG CACCATGCAA CTTTTTCACC TCTGCCTAAT CATCTCATGT TCATGTCCTA	1860
CTGTTCAAGC CTCCAAGCTG TGCCTTGGGT GGCTTGGGG CATGGACATT GACCCGTATA	1920
AAGAATTGG AGCTTCTGTG GAGTTACTCT CTTTTTGCC TTCTGACTTC TTTCTTCTA	1980
TTCGAGATCT CCTCGACACC GCCTCAGCTC TATATCGGGAA GGCTTAGAG TCTCCGGAAC	2040
ATTGTTCTCC TCATCATACA GCACTCAGGC AAGCTATTCT GTGTTGGGT GAGTTGATGA	2100
ATCTGGCAC CTGGGTGGGA AGTAATTGG AAGACCCAGC ATCCAGGAA TTAGTAGTCA	2160
GCTATGTCAA TGTTAATATG GGCCTAAAAA TCAGACAAC ACTGTGGTTT CACATTCTCCT	2220
GTCTTACTTT TGGAAGAGAA ACTGTTCTTG AGTATTGGT GTCTTGGGA GTGTGGATTG	2280
GCACTCCTCC TGCTTACAGA CCACCAAATG CCCCTATCTT ATCAACACTT CCGGAAACTA	2340
CTGTTGTTAG ACGACGAGGC AGGTCCCTA GAAGAAGAAC TCCCTGCCT CGCAGACGAA	2400
GGTCTCAATC GCCGCGTCGC AGAAGATCTC AATCTCGGGAA ATCTCAATGT TAGTATCCCT	2460
TGGACTCATA AGGTGGGAAA CTTTACTGGG CTTTATTCTT CTACTGTACC TGTCTTTAAT	2520
CCTGAGTGGC AAACTCCCTC CTTTCCCTCAC ATTCAATTAC AGGAGGACAT TATTAATAGA	2580

TGTCAACAAT ATGTGGGCC C TCTTACAGTT AATGAAAAAA GGAGATTAAA ATTAAATTATG	2640
CCTGCTAGGT TCTATCCTAA CCTTACCAAA TATTTGCCAT TGGACAAAGG CATTAAACCA	2700
TATTATCCTG AACATGCAGT TAATCATTAC TTCAAAACTA GGCATTATTT ACATACTCTG	2760
TGGAAGGCGG GCATTCTATA TAAGAGAGAA ACTACACGCA GTGCCTCATT CTGTGGGTCA	2820
CCATATTCTT GGGAACAGA GCTACAGCAT GGGAGGTTGG TCTTCAAAC CTCGACAAGG	2880
CATGGGGACG AATCTTCTG TTCCAATCC TCTGGGATTC TTTCCCGATC ACCAGTTGGA	2940
CCCTGCGTTC GGAGCCAATC CACACAATCC CGATTGGGAC TTCAACCCCCA ACAAGGATCA	3000
TTGGCCAGAG GCAAATCAGG TAGGAGCGGG AGCATTGGG CCAGGGTTCA CCCCACCACA	3060
CGGCGGTCTT TTGGGGTGA GCCCCCAGGC TCAGGGCGTA TTGACAACCG TGCCAGTAGC	3120
ACCTCCCTCCT GCCTCCACCA ATCGCAGTC AGGAAGACAG CCTACTCCCA TCTCTCCACC	3180
TCTAAAGAGAC AGTCATCCTC AGGCCATGCA GTGG	3214

(2) INFORMATION FOR SEQ ID NO: 295:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 295:

AACTCCACAA CATTCCACCA AGCTCTGCTA GACCCCAGAG TGAGGGGCCT ATACTTTCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCCTGCA CCGAACATGG AGAACACAAC ATCAGGATTC	130
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TACACTCGTG GTGGACTTCT CTCAATTTC TAGGGGCAGC ACCCACGTGT	300
CTTGGCCAAA ATTTCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCCTGGTT ATCGTTGGAT GTGCTGCGG CGTTTTATCA TATTCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTCTG GACTACCAAG GTATGTTGTC TGTTTGTCT	480
CTACTTCCAA GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCCCTGCT	540
CAAGGAACCT CTATGTTCC CTCTTCTTGC TGTACAAAAC CTTGGACGG AAACTGCACT	600
TGTATTCCCA TCCCATCATC TTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCAAGT GGTTCTGAGG GCTTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780

TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CCAATAAAAC CAAACGTTGG GGCTATTCCC TTAATTCAT GGGATATGTA ATTGGATGTT	900
GGGGTACTTT ACCGCAAGAA CATATTGTAC TAAAAATCAA GCAATGTTT CGAAAACCTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAGAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAAGC TTTCACTTTC TCGCCAACCTT ACAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCT ATTGCCATC GCCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCCTGGCAG CCTGTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AACTTATCGG AACCGACAAC TCTGTTGTCC TCTCTCGGAA ATACACCTCC TTTCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG CCTCTATCGT CCCCTCTTC	1500
ATCTACCGTT CGGGCCGACC ACGGGGCGCA CCTCTCTTAA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCC CTTCACCTCT GCACGTGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACATAAG AGCACTTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTAAGG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGGT TAAAGGTCTT TGTACTGGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTACCA GCACCATGCA ACTTTTCAC CTCTGCCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTGGG GCATGGACAT TGACCCGTAT	1920
AAAGAATTG GAGCTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTTCTTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTCAGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGCTCAC CTCAACCATAAC CGCACTCAGG CAAGCTATTTC TGTGTTGGCG TGAGTTGATG	2100
AATCTGGCCA CCTGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGGAA ATTAGTAGTC	2160
AGCTATGTCA ATGTTAATAT CGGCCTAAAA ATCAGACAAC TACTGTGGTT TCACATTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTG TGCTTTGG AGTGTGGATT	2280
CGCACTCCTC CTGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTATCTTAA	2520
TCCTGAGTGG CAAACTCCCT CCTTCTCA CATTCAATTAA CAGGAGGACA TTATTAATAG	2580
ATGTCAACAA TATGTGGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AGTTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATCTGCC TTGGACAAAG GCATTAACCC	2700
ATATTATCCT GAACATGCAG TTAATCATTA CTTCAAAACT AGGCATTATT TACATACTCT	2760

GTGGAAGGCG GGCATTCTAT ATAAGAGAGA AACTACGCGC AGCGCCTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGAC GAATCTTCT GTTCCAATC CTCTGGGATT CTTCCCGAT CACCAGTTGG	2940
ACCTGCGTT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC ACAAAGGATC	3000
ACTGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTGGC GCCAGGGTTC ACCCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGTAG	3120
CACCTCCTCC TGCCCTCAC AATCGGCAGT CAGGAAGACAA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 296:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 296:

AACTCCACAA CATTCCACCA AGCTGTGCTA GATCCCAGAG TGAGGGGCCT ATATCTTCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTGAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCTGCA CCGAACATGG AGAACACAAAC ATCAGGATTG	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAGAAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCCAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCTGGCT ATCGCTGGAT GTGTCGCGG CGTTTATCA TATTCCCTTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGTG GGTTCTTCTG GACTACCAAG GTATGTTGCC CGTTGTCCT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTCC CTCCCTGTTGC TGTACAAAC CTTCGGACGG AAACCTGCACT	600
TGTATTCCA TCCCCATCATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCCT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTCATAAAAC CAAACGTTGG GGCTACTCCC TAAACTTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAC TAAAAATCAA GCAATGTTT CGGAAGCTGC	960

CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGGAT TGTGGGTCTT TTGGGTTTG	1020
CTGCCCCTTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATAACAT	1080
CTAACGAGGC TTTCACTTTTC TCGCCAACCTT ACAAGGCCTT TCTGTGTAAA CAATATCTGC	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCC ATTGGCAAT CGGGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTGCG TCGCAGCCGG TCTGGAGCGA	1320
AACTTATCGG GACTGACAAC TCTGTTGTCC TCTCTCGGAA ATACACCTCC TTCCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG CCTCTACCGT CCCCTTCTTC	1500
ATCTGCCGTT CCGGCCGACC ACGGGGCGCG CCTCTCTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACCTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
GATGTCAACG ACCGACCTTG AGGCATATTT CAAGACTGT TTGTTAAAG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGGT TAATGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCCTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTGGG TGGCTTAGGG GCATGGACAT TGACACGTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTCCCTTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTTGCT CTGCATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAAC AGCACTCAGG CAAGCTATTG TGTGTGGGG TGAGTTGATG	2100
AATCTGGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGGA ATTGGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCCTAAAA ATCAGACAC TATTGTGGTT TCACATTCC	2220
TGTCTTACTT TTGGAAGAGA AACGGTTCTT GAGTATTGG TATCTGTTGG AGTGTGGATT	2280
CGCACTCCTC AAGCCTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTAAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGAA ACTTTACTGG TCTCTATTCT TCTACTGTAC CTGTCTTAA	2520
TCCTGAGTGG CAAACTCCCT CCTTTCTAA TATTCAATTAA CAGGAGGATA TTATTAATAG	2580
ATGTCAACAA TATGTAGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCC TTGGATAAAG GTATTAACCC	2700
TTATTATCCT GAACATGCAG TTAATCATTA TTTCAAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAGAGAGA AACTACACGT AGTGCCTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940

ACCCCTGCATT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCC AACAAAGGATC	3000
ATTGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTGG GCCAGGGTTC ACTCCACCAC	3060
ACGGCGGTCT TTTGGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGCAG	3120
CGCCTCCTCC TGCCCTAAC AATCGGCAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 297:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 297:

AACTCCACAA CATTCCACCA AGCTGTGCTA GATCCCAGAG TGAGGGGCCT ATATCTTCCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTGAAC CCTGTTCCGA CTACTGCCTC ACCCATATCG	120
TCAATCTTCT CGAGGACTGG GGACCCCTGCA CCGAACATGG AGAACACAAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC ACCCACGTGT	300
CCTGGCCCAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCCCTTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCCCTGCT	540
CAAGGAACCT CTATGTTCC CTCCCTGTC TGTACAAAAC CTTCGGACGG AAAACTGCACT	600
TGTATTCCCA TCCCACATC CTGGGCTTTC GCAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTCTGAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAACATC	780
TTGAGTCCTT TTTTACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTCATAAAAAC CAAACGTTGG GGCTACTCCC TTAACCTCAT GGGATATGTA ATTGGAAGTT	900
GGGGTACTTT ACCACAGGAA CATATTGTAC TAAAAATCAA GCAATGTTT CGGAAGCTGC	960
CTGTAAATAG ACCTATTGAT TGGAAAGTAT GTCAAAGGAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGCTATCCTG CCTTGATGCC TTTATATGCA TGTATACAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACCTT ACAAGGCCTT TCTGTGTAAA CAATATCTGC	1140

ACCTTTACCC CGTTGCCCGG CAACGGTCAG GTCTCTGCCA AGTGTGCT GACGCAACCC	1200
CCACTGGATG GGGCTTGGCC ATTGGCCAAT CGGGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCAG CTTGTTTGC TCGCAGCCGG TCTGGAGCGA	1320
AACTTATCGG GACTGACAAC TCTGTTGTCC TCTCTCGGAA ATACACCTCC TTCCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTCTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG CCTCTACCCT CCCCTTCTTC	1500
ATCTGCCGTT CGGGCCGACC ACGGGGCGCG CCTCTCTTA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACCTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCAGGTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
GATGTCAACG ACCGACCTTG AGGCATATT CAAAGACTGT TTGTTAAAG ACTGGGAGGA	1740
GTTGGGGGAG GAGATTAGGT TAATGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCCTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTAGGG GCATGGACAT TGACACGTAT	1920
AAAGAATTG GAGCTCTGT GGAGTTACTC TCTTTTTGC CTTCTGACTT CTTCCCTTCT	1980
ATTCGAGATC TCCTCGACAC CGCCTTGCT CTGCATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAAC AGCACTCAGG CAAGCTATTG TGTGTTGGGG TGAGTTGATG	2100
AATCTGGCCA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGGA ATTGGTAGTC	2160
AGCTATGTCA ATGTTAATAT GGGCTAAAA ATCAGACAA TATTGTGGTT TCACATTTC	2220
TGTCTTACTT TTGGAAGAGA AACGGTTCTT GAGTATTGG TATCTGTTGG AGTGTGGATT	2280
CGCACTCCTC AAGCCTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGGC TCGCAGACGA	2400
AGGTCTAAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGGAA ACTTTACTGG TCTCTATTCT TCTACTGTAC CTGTCTTAA	2520
TCCTGAGTGG CAAACTCCCT CCTTTCTAA TATTCAATTAA CAGGAGGATA TTATTAATAG	2580
ATGTCAACAA TATGTAGGCC CTCTTACAGT TAATGAAAAA AGGAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTCTATCCTA ACCTTACCAA ATATTTGCC TTGGATAAAG GTATTAACCC	2700
TTATTATCCT GAACATGCAG TTAATCATTAA TTTCAAAACT AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATTCTAT ATAAGAGAGA AACTACACGT AGTGCCTCAT TTTGTGGGT	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGACAAG	2880
GCATGGGGAC GAATCTTCT GTTCCCAATC CTCTGGGATT CTTTCCCGAT CACCAGTTGG	2940
ACCTGCATT CGGAGCCAAC TCAAACAATC CAGATTGGGA CTTCAACCCCC AACAAAGGATC	3000
ATTGGCCAGA GGCAAATCAG GTAGGAGCGG GAGCAATTGG GCCAGGGTTC ACTCCACCAC	3060
ACGGCGGTCT TTTGGGTGG AGCCCTCAGG CTCAGGGCAT ATTGACAACA GTGCCAGCAG	3120

CGCCTCCTCC TGCCTCTACC AATCGGGAGT CAGGAAGACA GCCTACTCCC ATCTCTCCAC 3180

CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG 3215

(2) INFORMATION FOR SEQ ID NO: 298:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 298:

AACTCCACCA CATTCCACCA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCCCT 60  
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCCT ACCCATATCG 120  
TCAATCTTCT CGAGGACTGG GGACCCCTGCG CCGAACATGG AGAACACAAC ATCAGGATTC 180  
CTAGGACCCC TGCTCGTGT ACAGGCAGGG TTTTTCTTGT TGACAAGAAT CCTCACAATA 240  
CCACAGAGTC TAGACTCGTG GACTTCTCTC AATTTCTAG GGGGAGCACC CACGTGTCC 300  
GGCCAAAATT CGCAGTCCCC AACCTCCAAT CACTCACCAA CCTCTTGTCC TCCAATTGT 360  
CCTGGCTATC GCTGGATGTG TCTGCGCGT TTTATCATAT CCTCTTGTAT CCTGCTGCTA 420  
TGCCTCATCT TCTTGTGTC TCTTCTGGAC TACCAAGGTA TGTTGCCGT TTGTCCTCTA 480  
CTTCCAGGAA CATCAACTAC CAGCACGGGA CCATGCAAGA CCTGCACGAT TCCTGCTCAA 540  
GGAACCTCTA TGTTCCCTC TTGTTGCTGT ACAAAACCTT CGGACGGAAA TTGCACTTGT 600  
ATTCCCATCC CGTCATCTG GGCTTCGCA AGATTCTAT GGGAGTGGC CTCAGTCCGT 660  
TTCTCCTGGC TCAGTTACT AGTGCCATT GTTCAGTGGT TCGCAGGGCT TTCCCCCACT 720  
GTTTGGCTTT CAGTTATATG GATGATGTGG TATTGGGGC CAAGTCTGTA CAACATCTG 780  
AGTCCCTTTA TACCTCTATT ACCAATTTC TTGTTGCTTT GGGTATAACAT TTGAACCCTA 840  
ATAAAACCAA ACGTTGGGGC TACTCCCTA ACTTCATGGG ATATGTAATT GGAAGTTGGG 900  
GTACGTTACC ACAGGAACAT ATTGTACAAA AAATCAAGCA ATGTTTCGG AAACTGCCTG 960  
TAAATAGACC TATTGATTGG AAAGTATGTC AAAGAATTGT GGGTCTTTG GGCTTGCTG 1020  
CCCCTTTAC ACAATGTGGT TATCCTGCCT TGATGCCTTT ATATGCATGT ATACAAGCTA 1080  
AGCAGGCTTT TACTTTCTCG TCAACTTACA AGGCCTTCT GTGTAACAA TATCTGCACC 1140  
TTTACCCCGT TGCCCGGCAA CGGTCAGGTC TCTGCCAAGT GTTTGCTGAC GCAACCCCCA 1200  
CTGGATGGGG CTTGGCCATA GGCCATCGGC GCATGCGTGG AACCTTGTG GCTCCTCTGC 1260

CGATCCATACT	TGCGGAACTC	CTAGCAGCTT	GTTTGCTCG	CAGCCGGTCT	GGAGCGAAC	1320
TTATCGGGAC	TGACAACACTCT	GTTGTCCTCT	CTCGGAAATA	CACCTCCTTC	CCATGGCTGC	1380
TCGGATGTGC	TGCCAACTGG	ATCCTGCGCG	GGACGTCCTT	TGTCTACGTC	CCGTCGGCGC	1440
TGAATCCCAC	GGACGACCCCG	TCTCGGGGTC	GTTTGGGCCT	CTACCGTCCC	CTTCTTCATC	1500
TGCCGTTCCG	GCCGACCACG	GGCGCACCT	CTCTTACGC	GGTCTCCCCG	TCTGTGCCTT	1560
CTCATCTGCC	GGACCGTGTG	CACTTCGCTT	CACCTCTGCA	CGTCGCATGG	AGACCACCGT	1620
GAACGCCCAT	CAGGTGTTGC	CCAAGGTCTT	ATATAAGAGG	ACTCTTGGAC	TTTCAGCAAT	1680
GTCAACGACC	GACCTTGAGG	CATACTTCAA	AGACTGTTG	TTTAAGGACT	GGGAGGAGTT	1740
GGGGGAGGAA	CTTAGGTTAA	TGATCTTGT	ACTAGGAGGC	TGTAGGCATA	AATTGGTCTG	1800
TTCACCAGCA	CCATGCAACT	TTTCACCTC	TGCCTAATCA	TCTCTTGTTC	ATGTCCTACT	1860
GTTCAGCCT	CCAAGCTGTG	CCTTGGGTGG	CTTTAGGACA	TGGACATTGA	CCCATATAAA	1920
GAATTGGAG	CTTCTGTGGA	GTTACTCTCT	TTTTTGCCTT	CTGACTTCTT	TCCTTCTATT	1980
CGAGATCTCC	TCGACACCGC	CTCTGCTCTG	TATCGGGAGG	CCCTAGAGTC	TCCGGAGCAT	2040
TGTACACCTC	ACCATACAGC	ACTCAGGCAA	GCTATTCTGT	GTTGGGGTGA	GTTGATGAAC	2100
CTGGCCACCT	GGGTGGGAAG	TAATTGGAA	GATCCAACAT	CCAGGGAAAGC	AGTAGTCAGC	2160
TATGTCAATG	TTAATATGGG	CCTAAAACTC	AGACAACAT	TGTGGTTCA	CATTTCTGT	2220
CTTACTTTG	GAAGAGATAC	TGTTCTTGAG	TATTTGGTGT	CTTTGGAGT	GTGGATTCGC	2280
ACTCCTACCG	CTTACAGACC	ACCAAAATGCC	CCTATCTTAT	CAACACTTCC	GGAAACTACT	2340
GTGTTAGAC	GACCGAGGAG	GTCCCCTAGA	AGAAGAACTC	CCTCGCCTCG	CAGACGAAGG	2400
TCTCAATCGC	CGCGTCCGAG	AAGATCTCAA	TCTCGGGAAC	CTCAATGTTA	ATGTCCTTG	2460
GACTCATAAG	GTGGGAAACT	TTACAGGACT	TTACTCTTCT	ACTGTACCTG	TCTTTAATCC	2520
TGAGTGGCAA	ACTCCCTCCT	TTCTAACAT	TCATTTACAG	GAGGACATTA	TTGATAGATG	2580
TCAACAAATAT	GTGGGCCCTC	TTACAGTTAA	TGAAAAAAGG	AGATTAATAAT	TAATTATGCC	2640
TGCTAGGTTT	TATCCAAACC	TTACCAAATA	TTTGCCTTG	GATAAAGGCA	TTAAACCTTA	2700
TTATCCTGAA	CATGCAGTTA	ATCATTACTT	TCAAACTAGG	CATTATTTAC	ATACTCTGTG	2760
GAAGGCTGGC	ATTCTATATA	AGAGAGAAAC	TACCCGCAGC	GCTTCATTTT	GTGGTCACC	2820
ATATTCTTGG	GAACAAGAGC	TACAGCATGG	GAGGTTGGTC	TTCCAAACCT	CGACAAGGCA	2880
TGGGGACGAA	TCTTCTGTT	CCCAATCCTC	TGGGATTCTT	TCCCGATCAC	CAGTTGGACC	2940
CTGCGTTCGG	AGCCAACCTCA	AAACATCCAG	ATTGGGACTT	CAACCCCAAC	AAGGATCATT	3000
GGCCAGAGGC	CAATCAGGTA	GGAGTGGGAG	CATTCGGGCC	AGGGTTCAC	CCACCAACACG	3060
GCGGTCTTTT	GGGGTGGAGC	CCTCAGGCTC	AGGGCATATT	GACAACAGTG	CCAGCAGCGC	3120
CTCCTCCTGC	CTCTACCAAT	CGGCAGTCAG	GAAGACAGCC	AACTCCCAC	TCTCCACCTC	3180
TAAGAGACAG	TCATCCTCAG	GCCATGCAGT	GG			3212

(2) INFORMATION FOR SEQ ID NO: 299:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 299;

AACTCCACAA CATTCCAACA AGCTCTGCAG GATCCCAGAG TCAGGGTCCT TTATTTCC	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC TCTCATTTCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGTA ACGAACATGG AGAACACAAAC ATCAGGATT	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTTCTTGT TGACAAAAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCATTTC TAGGGGGAGC ACCCGTGTGT	300
CCTGGCCAAA ATTGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCAG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGTG GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCCCTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTACAAAAC CTTGGACGG AAAACTGCACT	600
TGTATTCCCA TCCCCATCATC CTGGGCTTTC GTAAGATTC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGCGCCA TTTGTTCACT GGTTCTAGG GCTTTCCCCC	720
ACTGTTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GCCCAAGTCT GTACAAACATC	780
TTGAGTCCCT TTATAACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTAATAAAAC CAAAAGATGG GGCTATTCCC TTAACCTCAT GGGCTATGTA ATTGGAAAGTT	900
GGGGTACCTT ACCACAAGAA CATATTGTAC TAAAAATCAC ACAATGTTT CGAAAACCTC	960
CTGTTAATAG GCCTATTGAT TGGAAAGTGT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGGTATCCTG CCTTAATGCC CTTGTATGCC TGTATTCAAG	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACTT ATAAGGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCTG GTCTTGCCTA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATGGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCGG CTTGTTTGC TCGCAGCCGG TCTGGAGCAA	1320
ACATTATCGG AACCGACAAAC TCTGTCGTCC TCTCTCGGAA ATACACATCC TTTCCATGGC	1380
TGCTCGGGTG TGCTGCCAAC TGGATCCTAC GCGGGACGTC CTTTGTGTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGCG GCGGTTGGG GCTCTACCGT CCCCTTCTTT	1500

GTCTGCGGTT	CCGGCCAACC	ACGGGGCGCA	CCTCTCTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAAACCAC	1620
CGTGAACGCC	CACATGGTCT	TGCCCAAGGT	CTTGCATAAG	AGAACTCTTG	GACTCTCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATATT	CAAAGACTGT	GTGTTCAAAG	ACTGGGAGGA	1740
GTTGGGGAG	GAGGTTAGAT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCTAA	TCATCTCATG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTGGG	GCATGGACAT	TGACCCTTAT	1920
AAAGAATTG	GAGCTCTGT	GGAGTTACTC	TCTTTTTGC	CTTCTGATTT	CTTTCCATCT	1980
ATTCGAGACC	TCCTCGACAC	CGCCTCAGCT	CTGTATCGGG	AGGCCTTAGA	GTCTCCGGAG	2040
CATTGTTCAC	CTCACCAAC	AGCACTCAGG	CAAGCTGTC	TGTGTTGGGG	TGAGTTAACG	2100
AATCTGGCTA	CCTGGGTGGG	AAGTAATTG	GAAGACCCAG	CATCAAGAGA	ATTGGTAGTC	2160
AGTTATGTCA	ATGTTAATAT	GGGCCTAAAA	ATCAGGCAAC	TGTTGTGGTT	TCATATTCC	2220
TGTCTTACTT	TTGGAAGAGA	AACTGTTCTT	GAGTACTTGG	TGTCCTTGG	AGTGTGGATT	2280
CGCACTCCTC	CCGCTTACAG	ACCACCAAAT	GCCCCTATCT	TATCAACACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGAAGAGG	CAGGTCCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCGGG	AATCCAATG	TTAGTATCCC	2460
TTGGACTCAT	AAGGTGGAA	ACTTTACTGG	GCTTTATTCT	TCTACTGTAC	CTGTCTTAA	2520
TCCTGAATGG	CAAACCTCCCT	CTTTCTGA	CATTCAATTG	CAGGAGGACA	TTATTAATAG	2580
ATGTCAACAA	TATGTGGGCC	CTCTTACAGT	TAATGAAAAA	AGAAGATTAA	AATTAATTAT	2640
GCCTGCTAGG	TTTTATCCTA	ACCTTACTAA	ATATTGCC	TTAGACAAAG	GCATTAACCC	2700
TTATTATCCA	GAACAGACAG	TTAATCATT	CTTCAAAACT	AGGCATTATT	TGCATACTCT	2760
GTGGAAGGCT	GGTAGTCTAT	ATAAGAGAGA	AACTACACGC	AGCGCCTCAT	TTTGTGGGTC	2820
ACCATATTCT	TGGGAACAAG	AGCTACAGCA	TGGGAGGTTG	GTCTCAAAA	CCTCGGAAAG	2880
GCATGGGGAC	GAATCTTCG	GTACCCAATC	CTCTGGGATT	CTTCCCGAT	CACCAGTTGG	2940
ACCCCTGCGTT	CGGAGCCAAC	TCAAACAATC	CCGATTGGGA	CTTCACCCCC	AACAAGGATC	3000
ACTGGCCAGA	GGCAAATCAG	GTAGGAGCGG	GAGCATTGG	GCCAGGGTTC	ACCCCAACCAC	3060
ACGGAGGTCT	TTTGGGGTGG	AGCCCTCAGG	CCCAGGGCAT	ATTGACAACA	GTGCCAGCAG	3120
CTCCTCCTTC	TGCCTCCACC	AATCGGCAGT	CAGGAAGACA	GCCTACGCC	ATCTCTCCAC	3180
CTCTAAGAGA	CAGTCATCCT	CAGGCCATGC	AGTGG			3215

(2) INFORMATION FOR SEQ ID NO: 300:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 300:

AACTCCACAA CATTCCAACA AGCTCTGCTA GATCCCAGAG TGAGGGGCCT ATATTTCTT	60
GCTGGTGGCT CCAGTTCCGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC TCTCATTTCG	120
TCAATCTTCT CGAGGACTGG GGACCCTGTA ACGAACATGG AGAACACAAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGGGGGG TTTTCTTGT TGACAAGAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGGG GTGGACTTCT CTCAATTTC TAGGGGAAGC ACCAAGGTGT	300
CCTGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCTGGCT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTTCTG GACTACCAAG GTATGTTGCC CGTTGTCCT	480
CTACTTCCAG GAACATCAAC TACCAGCACG GGACCATGCA AGACCTGCAC GATTCTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTACAAAAC CTTGGACGG AAAACTGCACT	600
TGTATTCCA TCCCATCATC CTGGGCTTTC GTAAGATTCC TATGGGAGTG GGCCTCAGTC	660
CGTTTCTCCT GGCTCAGTTT ACTAGGCCA TTTGTTCACT GTTCTCGTAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCTCT ATTACCAATT TTCTTTGTC TTTGGGTATA CATTGAAACC	840
CTAATAAGAC CAAAAGATGG GGCTATTCCC TTAACCTCAT GGGCTATGTA ATTGGAAAGTT	900
GGGGTACCTT ACCACAAGAA CATATTGTAC TAAAAATCAA ACAATGTTT CGAAAACCTTC	960
CTGTAAATAG GCCTATTGAT TGGAAGGTCT GCCAAAGAAT TGTGGGTCTT TTGGGATTG	1020
CTGCCCTTT TACACAATGT GGATATCCTG CCTTAATGCC TTTGTATGCA TGTATTCAAG	1080
CTAAGCAAGC TTTCACTTT TCGTCAACTT ACAAAAGCCTT TCTGTGTAAA CAATATCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGTCTG GTCTCTGCCA AGTGTGGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATTGGCAATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCCTAGCAG CTTGTTTGC TCGCAGCCGG TCTGGAGCAA	1320
AACTTATCGG AACTGACAAC TCTGTCGTCC TCTCTCGCAA ATACACATCC TTTCCATGGC	1380
TGCTCGGCTG TGCTGCCAAC TGGATCCTAC GAGGGACGTC CTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCGTCTCGGG GCCGTTGGG GATCTACCGT CCCCTTCTTC	1500
GTCTGCGGTT CGGGCAACC ACGGGGCGCA CCTCTCTTCA CGCGGTCTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCCT GTGCACCTCG CTTCACCTCT GCACGTGCA TGGAGACCAC	1620
CGTGAACGCC CACATGGTAT TGCCCAAGGT CTTGCATAAG AGGACTCTTG GACTCTCAGC	1680

GATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT GTATTAAAG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCATG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCCTAT	1920
AAAGAATTG GAGCTTCTGT GGAGTTACTC TCTTTTTGC CTTCTGATTT CTTCCATCT	1980
ATTCGAGACC TCCTCGACAC CGCCTCAGCT CTGTATCGGG AGGCCTTAGA GTCTCCGGAA	2040
CATTGTTCAC CTCACCATAc AGCACTCAGG CAAGCTGTT TGTGTTGGG TGAGTTAATG	2100
AATCTGGCTA CCTGGGTGGG AAGTAATTG GAAGACCCAG CATCCAGGG AATTAGTGGTC	2160
AGTTATGTCA ACATTAATAT GGGCCTAAAA ATCAGACAAC TATTGTGGTT TCACATTCC	2220
TGTCTTACTT TTGGAAGAGA AACTGTTCTT GAGTATTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CCGCTTACAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGTCGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CACCGCGTCG CAGAAGATCT CAATCTGGG AATCCCAATG TTAGTATCCC	2460
TTGGACTCAT AAGGTGGAA ACTTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTTAA	2520
TCCTGAATGG CAAACTCCCT CTTTCCTGA CATTCAATTG CAGGAGGACÀ TTATTAATAG	2580
ATGTCAACAA TATGTGGCC CTCTTACAGT TAATGAAAAA AGAAGATTAA AATTAATTAT	2640
GCCTGCTAGG TTTTATCCTA ACCTTACCAA ATATTTGCCCT TAGATAAAAG GCATTAACC	2700
TTATTATCCT GAACATGCAG TTAATCATTAA CTTCAAAACA AGGCATTATT TACATACTCT	2760
GTGGAAGGCT GGCATCTTAT ATAAAAGAGA AACTACACGC AGTGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAAG AGCTACAGCA TGGGAGGTTG GTCTTCCAAA CCTCGGAAAG	2880
GCATGGGAC GAATCTTCT GTTCCAATC CTCTGGGATT CTTCCCGAT CACCAGTTGG	2940
ACCCTGCATT CGGAGCCAAC TCAAACATC CAGATTGGGA CTTCAACCCC AACAAAGGATC	3000
AATGCCAGA GGCAAATCAG GTAGGAGCGG GAGCATTGG GCCAGGGTTC ACCCCACCAC	3060
ACGGAGGTCT TTTGGGTGG AGCCCTCAGG CACAAGGCAT ATTGACAACA CTGCCAGCAG	3120
CTCCTCCTCC TGCCTCCACC AATCGGCAGT CAGGAAGACA GCCTACGCC ATCTCTCCAC	3180
CTCTAAGAGA CAGTCATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 301:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3161 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 301:

AATTCCACAA CCTTCCACCA AACTCTACAA GATCCCCCTG CTGGTGGCTC CAGTCAGGA 60  
ACAGTAAACC CTGTTCCGAC TACTGTCTCT CACATATCGT CAATCTTCAC GAGGATTGGG 120  
GACCCCTGCAC TGAACATGGA GAACATCACA TCAGGATTCC TAGGACCCCT GCTCGTGT 180  
CAGGCCGGGT TTTTCTTGTG GACAAGAAC CTCACAATAAC CGCAGAGTCT AGACTCGTGG 240  
TGGACTTCTC TCAATTCTTCT AGGGGAACT ACCGTGTGTC TTGGCCAAAA TTCGCAGTCC 300  
CCAACCTCCA ATCACTCACC AACCTCCTGT CCTCCAACCTT GTCCCTGGTTA TCGCTGGATG 360  
TGTCTGCGC GTTTTATCAT CTTCCCTTTC ATCCTGCTGC TATGCCTCAT CTTCTTGTG 420  
GTTCTTCTGG ACTATCAAGG TATGTTGCCC GTTTGTCCTC TAATTCCAGG ATCTTCAACC 480  
ACCAGCACGG GACCATGCAG GACCTGCACG ACTCCTGCTC AAGGCAACTC TATGTATCCC 540  
TCCTGTTGCT GTACCAAACC TTGGGACGGG AATTGCACCT GTATTCCCAT CCCATCATCT 600  
TGGGCTTCG GAAAATTCCCT ATGGGAGTGG GCCTCAGCCC GTTCTCCTG GCTCAGTTA 660  
CTAGTGCCTAT TTGTTCAGTG GTTCGTAGGG CTTTCCCCCA CTGTTGGCT TTCAGTTATA 720  
TGGATGATGT GGTATTGGGG GCCAAGTCTG TACAGCATCT TGAGTCCCTT TTTACCGCTG 780  
TTACCAAATT TCTTTGTCT TTGGGCATAC ATTTAAACCC TAACAAAACA AAAAGATGGG 840  
GTTACTCTTT ACACCTCATG GGCTATGTCA TTGGATGTTA TGGGTCAATTG CCACAAGATC 900  
ACATCAGACA GAAAATCAA GAATGTTTA GAAAACCTCC TGTTAACAGG CCTATTGATT 960  
GGAAAGGCTG TCAACGAATT GTGGGTTTAT TGGGTTTGC TGCCCTTTT ACACAATGTG 1020  
GTTATCCTGC GTTGATGCCT TTGTTATGCAT GTATTCAATC TAAGCAGGCT TTCACTTTCT 1080  
CGCCAACTTA CAAGGCCTTT CTGTGTAAAC AATACCTGAA CCTTACCCCG TTGCCCGGC 1140  
AACGGCCAGG TCTGTGCCAA GTGTTGCTG ACGCAACCCC CACTGGCTGG GGCTTGGTCA 1200  
TGGGCCATCA GCGCATGCGT GGAACCTTTC GGGCTCCTCT GCCGATCCAT ACTGCGGAAC 1260  
TCCTAGCCGC TTGTTTGTCT CGCAGCAGGT CTGGAGCAAA CATTCTCGGG ACGGATAACT 1320  
TTGTTGTCCT ATCCCGAAA TATACATCGT TTCCATGGCT GCTAGGCTGT GCTGCCAACT 1380  
GGATCCTGAG CGGGACGTCC TTCGTTTACG TCCCGTCGGC GCTGAATCCA GCGGACGACC 1440  
CTTCTCGGGG CCGCTTGGGA CTCTCTCGTC CCCTTCTCCG TCTGCCGTGTT CGTCCGACCA 1500  
CGGGGGCGCAC CTCTCTTAC GCGGAACCCC CGTCTGTGCC TTCTCATCTG CCGGACCGTG 1560  
TGCACCTCGC TTCACCTCTG CACGTGCAT GGAGACCACC GTGAACGCC ACCAATTCTT 1620  
GCCCAAGGTC TTACATAAGA GGACTCTTGG ACTCTCAGCA ATGTCAACGA CCGACCTTGA 1680  
GGCATACTTC AAAGACTGTT TGTTAAAGA GTGGGAGGAG TTGGGGAGG AGATTAGATT 1740  
AAAGTTGTTT GTATTAGGAG GCTGTAGGCA TAAATTGGTC TGCGCACCAAG CACCATGCAA 1800  
CTTTTCACC TCTGCCTAAT CATCTCTTGT TCATGTCCCTA CTGTTCAAGC CTCCAAGCTG 1860

TGCCTTGGGT GGCTTTAGGA CATGGACATT GATCCTTATA AAGAATTGG AGCTTCTATG	1920
GAGTTGCTCT CGTTTTGCC TTCTGACTTC TATCCTTCAG TACGAGATCT TCTAGATACC	1980
GCCTCAGCTC TATATCGGGA AGCCTTAGAG TCTCCTGAGC ATTGTACACC TCATCATACT	2040
GCACTCAGGC AAGCAATTCT TTGCTGGGG GAATTAATGA CTCTAGCCAC CTGGGTGGGT	2100
GGTAATTGCA AAGATCCAAC ATCCAGGGAC CTAGTAGTCA GTTATGTTAA CACTAATATG	2160
GGCCTAAAGT TCAGGCAACT ATTGTGGTT CACGTTCTT GTCTCACTT TGGAAGAGAA	2220
ACAGTCGTAG AGTATTGGT GTCTTTGGA GTGTGGATTC GCACTCCTCA AGCTTATAGA	2280
CCACCAAATG CCCCTATCTT ATCAACACTT CCGGAGACTT GTGTTGTTAG ACGACGAGGC	2340
AGGTCCCCTA GAAGAAGAAC TCCCTCGCCT CGCAGACGAA GGTCTCAATC GCCGCGTCGC	2400
AGAAGATCTC AATCTCGGGA ATCTCAATGT TAGTATTCTT TGGAACATC AGGTGGAAA	2460
CTTTACGGGG CTTTATTCTT CTACTGTTCC TGTCTTTAAC CCTCATTGGA AAACACCCCTC	2520
TTTTCTAAT ATACATTAC ACCAAGACAT TATCAAAAAA TGTAAACAAT TTGTAGGCC	2580
ACTCACAGTC AATGAGAAAAA GAAGACTGCA ATTGATTATG CCTGTCAGGT TTTATCCAAT	2640
GGTTACCAAA TATTGCCAT TGGATAAGGG TATTAAACCG TATTATCCAG AACATCTAGT	2700
TAATCATTAC TTCCAAACCA GACATTATTT ACACACTCTA TGGAAGGCAG GTGTATTATA	2760
TAAGAGAGAA ACAACACATA GCGCCTCATT TTGTGGATCA CCATATTCTT GGGAAACAAGA	2820
GATACAGCAT GGGGCAGAAT CTTTCCACCA GCAATCCTCT GGGATTCTTT CCCGACCACC	2880
AGTTGGATCC AGCCTTCAGA GCAAACACCG CAAATCCAGA TTGGGACTTC AATCCCACAA	2940
AGGACACCTG GCCAGACGCC ACAAAGGTAG GAGCTGGAGC ATTCCGGCTG GGACTCACCC	3000
CACCGCACGG AGGCCTTTG GGGTGGAGCC CTCAGGCTCA GGGCATACTA CAGACCGTGC	3060
CAGCAAATCC GCCTCCTGCC TCTACCAATC GCCAGACAGG AAGGCAGCCT ACCCCTCTGT	3120
CTCCACCTT GAGAGACACT CATCCTCAGG CCATGCAGTG G	3161

(2) INFORMATION FOR SEQ ID NO: 302:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 302:

AACCTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATTCCCT

GCTGGTGGCT	CCAGTTCA GG AACAGTAAAC CCTGTTCCGA	CTACTGCCTC	TCACTTATCG	120		
TCAATCTCT	CGAGGGATTGG	GGACCCCTGCG	CTGAACATGG	AGAACATCAC	ATCAGGATT	180
CTAGGACCCC	TTCTCGTGT	TT ACAGGCGGGG	TTTTCTTGT	TGACAAGAAT	CCTCACAATA	240
CCGCAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGAAAC	TACCGTGTGT	300
CTTGGCCAAA	ATT CGCAGTC	CCC AACCTCC	AATCACTCAC	CAACCTCCTG	TCCTCCA ACT	360
TGT CCTGGTT	ATCGCTGGAT	GTGTCTGCGG	CGTTTTATCA	TCTTCCCTT	CATCCTGCTG	420
CTATGCCTCA	TCTTCTTGT	GGTTCTTCTG	GACTATCAAG	GTATGTTGCC	CGTTGTCCT	480
CTAATTCCAG	GATCCTCAAC	CACCAGCACG	GGACCATGCC	GAACCTGCAC	GACTCCTGCT	540
CAAGGAACCT	CTATGTATCC	CTCCTGTTGC	TGTACCAAAC	CTTCGGACGG	AAATTGCACC	600
TGTATTCCCA	TCCCATCATC	CTGGGTTTC	GGAAAATTCC	TATGGGAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCA GT	GGTTCGTAGG	GCTTTCCCC	720
ACTGTTGGC	TTTCAGTTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATC	780
TTGAGTCCCT	TTTTACCGCT	GTTACCAATT	TTCTTTGTC	TTTGGGTATA	CATTTAAACC	840
CTAACAAAAC	AAAGAGATGG	GGTTACTCTC	TAAATTTAT	GGGCTATGTC	ATTGGATGTT	900
ATGGGTCCCT	GCCACAAGAA	CACATCATA	AAAAAAATCAA	AGAATGTTTT	AGAAAACCTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GTCAACGAAT	TGTGGGTCTT	TTGGGTTTG	1020
CTGCCCTTT	TACTCAATGT	GGTTATCCTG	CTTTAATGCC	CTTGTATGCA	TGTATTCAAT	1080
CTAACGCAGG	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTGTGTAAA	CAATACCTGA	1140
ACCTTTACCC	CGTTGCCGGG	CAACGGCCAG	GTCTATGCCA	AGTGTGGCT	GACGCCAACCC	1200
CCACTGGCTG	GGGCTTGGCT	ATGGGCCATC	AGCGCATGCG	TGGAACCTTT	TCGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTGTTGC	TCGCAGCAGG	TCTGGAGCAA	1320
ACATTATCGG	GACTGATAAC	TCTGTTGTCC	TCTCCCGCAA	ATATACATCG	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GCGGGACGTC	CTTTGTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCGTCTCGGG	GTCGCTTGGG	ACTCTCTCGT	CCCCTTCTCC	1500
GTCTGCCGTT	CCGACCGACC	ACGGGGCGCA	CCTCTCTTA	CGCGGACTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCTGACCTT	GTGCACTTCG	CTTCACCTCT	GCACGTGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAAATAT	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCTCTGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTAAAG	ACTGGGAGGA	1740
GTTGGGGAG	GAGATTAGAT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCTAA	TCATCTCTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTGGG	GCATGGACAT	TGACCCCTAT	1920
AAAGAATTG	GAGCTACCGT	GGAGTTACTC	TCGTTTTGC	CTTCTGACTT	CTTCCCTTCA	1980
GTACGAGATC	TTCTAGATAC	CGCCTCAGCT	CTGTATCGGG	ATGCCTTAGA	GTCTCCTGAG	2040
CATTGTTCAC	CTCACCCATAC	TGCACTCAGG	CAAGCAATT	TTTGCTGGGG	GGAACTAATG	2100

ACTCTAGCTA CCTGGGTGGG TGTAAATTG GAAGATCCAG CATCTAGGGA CCTAGTAGTC	2160
AGTTATGTCA ACACATAAT GGGCCTAAAG TTCAGACAAC TCTTGTGGTT TCACATTCT	2220
TGTCTCATTT TTGGAAGAGA AACAGTTATA GAGTATTGG TGTCTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCC TATCAACACT TCCGGAGACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGAA ATTTACTGG GCTTTATTCT TCTACTGTAC CTGTCTTAA	2520
TCCTCATTGG AAAACACCAT CTTTCCTAA TATACATTAA CACCAAGACA TTATCAAAA	2580
ATGTGAACAG TTTGTAGGCC CACTCACAGT TAATGAGAAA AGAAGATTGC AATTGATCAT	2640
GCCTGCTAGG TTTTATCCA AGGTTACCAA ATATTTACCA TTGGATAAGG GTATTAACC	2700
TTATTATCCA GAACATCTAG TTAATCATTA CTTCCAAACT AGACACTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA AACAACACAT AGCCCTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAG ATCTACAGCA TGGGGCAGAA TCTTCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTGGGCT GGGTTTCACC CCACCGCACG GAGGCCTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACAAACTTTG CCAGCAAATC CGCCTCCTGC CTCCACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCTCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 303:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 303:

AACTCCACAA CTTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT ATATTCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCCGA CTACTGCCTC TCCCTTATCG	120
TCAATCTTCT CGAGGATTGG GGACCCGTG ACGAATATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC GAGGGGAAAC TACCGTGTGT	300

CTTGGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCA	360
TGT CCTGGTT ATCGCTGGAT GTGTCTGC GGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTTCTG GAGTATCAAG GTATGTTGCA CGTTTGTCT	480
CTAATTCCAG GAACAACAAAC AACCAAGTACG GGACCATGCA AAACCTGCAC GACTCCTGCT	540
CAAGGCAACT CTATGTTCC CTCATGTTGC TGTACCAAAA CTTGGATGG AAATTGCACC	600
TGTATTCCA TCCCATCGTC TTGGGCTTTC GCAAATACC TATGGGAGTG GGCCTCAGTC	660
CGTTCTCTT GGCTCAGTT ACTAGTGCCA TTTGTTCA GTTCTCGTAGG GCTTCCCCC	720
ACTGTTGGC TTTCAGCTAT ATGGATGATG TGGTATTGGG GGCCAAAGTCT GTACAGCATE	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTAACAAAAC AAAGAGATGG GGTTACTCTT TACATTTCAT GGGCTATGTC ATTGGATGTT	900
ATGGGTCTT GCCACAAGAA CACATCATAAC AAAAATCAA AGAATGTTT AGAAAAGTTC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTAT GTCAACGAAT TGTGGGTCTT TTAGGTTTG	1020
CTGCCCCTT CACACAATGT GGTTATCCTG CTTTAATGCC CTTGTATGCT TGTATTCAAT	1080
TTAAGCAGGC TTTCACTTTC TCGCCAACCT ACAAGGCCCT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGCCAG GTCTATGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGGT ATGGGCCATC AGCGCATGCG TGGAACCTTT TCGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CCTGTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACATTCTCGG GACGGATAAC TCTGTTGTT TCTCCCGCAA ATATACTCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCTTCTCGGG GCCGCTTGGG ACTCTCTCGT CCCCTCTCT	1500
GTCTGCCGTT TCGACCGACC ACGGGGCGCA CCTCTCTTAC CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTCACCTCT GCACGTGCCA TGGAGACCAC	1620
CGTGAACGCC CATCAGATCC TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCCCAGC	1680
AATGTCAACG ACCGACCTTG AGGCCTACTT CAAAGACTGT GTGTTTAAGG ACTGGGAGGA	1740
GCTGGGGAG GAGATTAGGT TAAAGGTCTT TGTATTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGGCACCA GCACCATGCA ACTTTTAC CTCCTGCCTAA TCATCTCTTG TACATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCCTAT	1920
AAAGAATTG GAGCTACTGT GGAGTTACTC TCGTTTTGC CTTCTGACTT CTTTCCTTCC	1980
GTACGAGATC TCCTAGACAC CGCCTCAGCT CTGTATCGGG AAGCCTTAGA GTCTCCTGAG	2040
CATTGTTAC CTCACCATAC TGCACTCAGG CAAGCAATTG TTTGCTGGGG GGAACATAATG	2100
ACTCTAGCTA CCTGGGTGGG TGTTAATTG GAAGATCCAG CATCTAGAGA CCTAGTAGTC	2160
AGTTATGTCA ACACAAATAT GGGCTTAAAG TTCAGGCAAC TCTTGTGGTT TCACATTCT	2220
TGTCTCACTT TTGGAAGAGA AACAGTTATA GAGTATTGG TGGCTTCGG AGTGTGGATT	2280

CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCC TATCAACACT TCCGGAGACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGAA ACTTTACGGG GTTTTATTCT TCTACTGTTC CTGTCTTAA	2520
CCCTCATTGG GAAACCCCCT CTTTCCTAA TATACATTAA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAG TTTGTAGGCC CACTCACAGT TAATGAGAAA AGAAGATTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA AGGTTACCAA ATATTTACCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAACATCTAG TTAATCATTA CTTCCAAACT AGACACTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA ACAACACAT AGCGCCTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGGCAGAA TCTATCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTCCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGAT GGAGCTGGAG	3000
CATTCGGGCT GGGACTCACC CCACCGCACG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACACACCGTG CCAGCAAATC CGCCTCCTGC CTCTACCAAT CGCCAGACAG	3120
GAAGGCAACC TACCCCTCTG TCTCCACCTT TGAGAGACAC TCATCCTCAG GCCGTGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 304:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 304:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAGG AACAGTAAAC CCTGTTCTGA CTACTGCCTC TCCCTTATCG	120
TCAATCTCCG CGAGGACTGG GGACCCCTGCA CTGAACATGG AGAACATCAC ATCAGGATTG	180
CTAGGACCCC TGCTCGTGT ACAGGGGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAAC TACCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATC	360
TGTCCTGGTT ATCGCTGGAT GTGTCTGGGG CGTTTATCA TCTTCCTCTT CATCCTGCTG	420

CTATGCCTCA	TCTTCTTGTG	GGTTCTTCTG	GACTATCAAG	GTATGTTGCC	CGTTTGTCC	480
CTAATTCCAG	GATCTTCAAC	AACCAGCACG	GGACCATGCA	GAACCTGCAC	GACTCCTGCT	540
CAAGGAACCT	CTATGTATCC	CTCCTGTTGC	TGTACCAAAC	CTTCGGACGG	AAATTGCACC	600
TGTATTCCA	TCCCACATCATC	TTGGGCTTTC	GGAAAATTCC	TATGGGAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTTCGTAGG	GCTTTCCCCC	720
ACTGTTGGC	TTTCAGTTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATC	780
TTGAGTCCCT	TTTTACCGCT	GTTACCAATT	TTCTTTGTC	TCTGGGTATA	CATTTAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTATTCCC	TAAACTTCAT	GGGTTACATA	ATTGGAAGTT	900
GGGGAACGTT	GCCACAAGAT	CATATTGTAC	AAAAGATCAA	AGAATGTTT	AGAAAACCTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GGCAACGAAT	TGTGGGTCTT	TTGGGCTTTG	1020
CTGCTCCATT	TACACAATGT	GGATATCCTG	CCTTAATGCC	TTTGTATGCC	TGTATACAAG	1080
CTAAACAGGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTAAGTAAA	CACTACATGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTGTGTTGCT	GACGCAACCC	1200
CCACTGGCTG	GGGCTTGGCA	ATAGGCAATC	AGCGCATGCG	TGGAACCATT	GTGGCTCC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTGTTGC	TCGCAGCCGG	TCTGGGGCAA	1320
AGCTCATCGG	AACTGACAAT	TCTGTTGTCC	TCTCGCGGAA	ATATAACATCG	TTTCCATGGC	1380
TGCTAGGTTG	TACTGCCAAC	TGGATCCTTC	GCAGGGACGTC	CTTGTTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTCG	CTTCACCTCT	GCACATTGCA	TGGAGACCAC	1620
CGTGAACGCC	CATCAGATTA	TGCCCAAGGT	TTTACATAAG	AGGACTCTTG	GACTCCCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTTAAGG	ACTGGGAGGA	1740
GCTGGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCCTGGG	TGGCTTAGG	GCATGGACAT	TGACCCCTTAT	1920
AAACAATTG	GAGCTACTGT	GGAGTTACTC	CCGTATTGTC	CTTCTGACTT	CTTTCTCTAC	1980
GTACGAGATC	TCCTAGATAC	CGCCTCAGCT	CTGTATCGGG	AAGCCTTAGA	GTCTCCTGAG	2040
CATTGTTCAC	CTCACCATAC	TGCACTCAGG	CAAGCAATT	TTTGCTGGGG	GGAACTAATG	2100
ACTCTAGCTA	CCTGGGTGGG	TGTTAATTG	GAAGATCCAG	CATCTAGAGA	CTTAGTAGTC	2160
AGTTATGTCA	ACACTAATAT	GGGCCTAAAG	TTCAGGCAAC	TCTTGTGGTT	TCACATTCT	2220
TGTCTCACTT	TTGGAAGAGA	AACAGTTATA	GAGTATTG	TGTCTTCCGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCTTATAG	ACCAACAAAT	GCCCCTATCC	TATCAACACT	TCCGGAGACT	2340
ACTGTTGTTA	CACGACCGAGG	CAGGTCCCCCT	AGAAGAAGAA	CTCCCTCGCC	TGCCAGACCA	2400

AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGGA ACTTACGGG GCTTTATTCT TCTACTGTTC CTGTCTTAA	2520
TCCTCATTGG AAAACACCTT CTTTCCTAA TATACATTAA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAA TTTGTAGGCC CACTCACAGT CAATGAGAAA AGAAGACTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA ATGTCACCAA ATATTTGCCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAGCATCTAG TTAATCATTA CTTCCAAACC AGACATTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA AACAAACACAT AGCGCCTCAT TTTGTGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGGCAGAA TCTTCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTGGGCT GGGTTTCACC CCACCGCACG GAGGTCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACATACCGTG CCAGCAAATC CGCCTCCTGC CTCTACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCTCTG TCTCCACCTT TGAGAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 305:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 305:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCAAGAG TGAGAGGCCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGTTCTGA CTACTGCCTC TCCCTTATCG	120
TCAATCTCCG CGAGGACTGG GGACCCCTGTG ACGATCATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT AGAGGCAGGGG TTTTCTTGT TGACAAGAAC CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGAAC TACCGTGTGT	300
CTTGGCCAAA ATTGCGAGTC CCCAACCTCC CATCACTCAC CAACCTCCTG TCCTCCAATT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TATTCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTCTG GACTATCAAG GTATGTTGCC CGTTTGTCT	480
CTAATTCCAG GTACTTCAC AACCAAGCACG GGACCATGCA GAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTATCC CTCCCTGTTGC TGTACCAAAC CTTGGACGG AAATTGCACC	600

TGTATTCCCA	TCCCATCATC	TTGGGCTTTC	GGAAAATTCC	TATGGCAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTTCGTAGG	GCTTTCCCCC	720
ACTGTTGGG	TTTCAGCTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATC	780
GTGAGTCCCT	TTATACCGCT	GTTACCAATT	TTCTTTGTC	TCTGGGTATA	CATTTAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTATTCCC	AAAACCCAT	GGGTTACATA	ATTGGAAGTT	900
GGGGAACGTT	GCCACAGGAT	CATATTGTAC	AAAAGATCAA	ACACTGTTT	AGAAAACCTTC	960
CTGTTAACAG	GCCTATTGAT	TGGAAAGTAT	GGCAACGAAT	TGTGGTCTT	TTGGGTTTTG	1020
CTGCTCCATT	TACACAATGT	GGTTATCCTG	CCTTAATGCC	TTTGTATGCC	TGTATACAAG	1080
CTAACACAGGC	TTTCACTTTC	TCGCCAACTT	ACAAGGCCTT	TCTAAGTAAA	CAGTACATGA	1140
ACCTTTACCC	CGTTGCTCGG	CAACGGCCTG	GTCTGTGCCA	AGTGTGTTGCT	GACGCAACCC	1200
CCACTGGCTG	GGGCTTGGCA	TAGGGCCATC	AGCGCATGCG	TGGAACCTTT	GAGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGTGTTGC	TCGCAGCAGG	TCTGGAGCAA	1320
ACATTATCGG	GACTGATAAC	TCTGTGTC	TATCGCGGAA	ATATACATCG	TTTCCATGGC	1380
TGCTAGGTTG	TACTGCCAAC	TGGATCCTTC	GCGGGACGTC	CTTTGTTAC	GTCCCGTCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCTCGGG	GCCGCTTGGG	ACTCTCTCGT	CCCCTCTCC	1500
GTCTGCCGTT	CCAGCCGACC	ACGGGGCGCA	CCTCTCTTA	CGCGGTCTCA	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGTCCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CATCAAAGTC	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCCCAGC	1680
AATGTCAACG	ACCGACCTTG	AGGCCTACTT	CAAAGACTGT	GTGTTAAGG	ACTGGGAGGA	1740
GCTGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGGCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCTAA	TCATCTCTG	TTCATGTCCC	1860
ACTGTTCAAG	CCTCCAGCT	GTGCCTTGGG	TGGCTTGGG	GCATGGACAT	TGACCCCTTAT	1920
AAAGAATTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTGC	CTTCTGACTT	CTTCCCTTCC	1980
GTAAGAGATC	TCCTAGACAC	CGCCTCAGCT	CTGTATCGAG	AAGCCTTAGA	GTCTCCTGAG	2040
CATTGGTCAC	CTCACCATAC	TGCACTCAGG	CAAGCCATTC	TCTGCTGGGG	GGAACTGATG	2100
ACTCTAGCAT	CCTGGGTGGG	TGATAATTG	GAAGATCCAG	CGTCTAGGGA	CCTAGTAGTC	2160
AGTTATGTTA	ACACTAATAT	GGGCCTAAAG	ATCAGGCAAC	TATTGTGGTT	TCATATATCT	2220
TGCCTTACTT	TTGGAGAGA	GACTGACTT	GAATATTGG	TCTCTTCGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCCTATAG	ACCACCAAAT	GCCCCTATCT	TATCAACACT	TCCGGAAACT	2340
ACTGTTGTTA	GACGACGGGA	CAGGTCCCT	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGGTCTCAAT	CGCCCGCTCG	CAGAAGATCT	CAATCTCGGG	AATCTCAATG	TTAGTATTCC	2460
TTGGACTCAT	AAGGTGGGGA	ACTTTACTGG	GCTTTATTCT	TCTACTGTAC	CTGTCTTTAA	2520
TCCTCATTGG	AAAACACCAC	CTTTCCCTAA	TATACATTAA	CACCAAGACA	TTATCAAAAA	2580

ATGTGAACAG TTTGTAGGCC CACTCACAGT TAATGAGAAA AGAAGATTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA AGGTTACCAA ATATTTACCA TTGGATAAGG GTATTAAACC	2700
TTATTATCCA GAACATCTAG TTAATCATTA CTTCCAAACT AGACACTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGAGA ACAACACAT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG ATCTACAGCA TGGGGCAGAA TCTATCCACC AGCAATCCTC	2880
TGGGATTCTT TCCC GACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTCGGGCT GGGTTTCACC CCACCGCACG GAGGCCTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT ACAAACTTG CCAGCAAATC CGCCTCCTGC CTCCACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCTCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 306:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 306:

AACTCCACAA CCTTCCACCA AACTCTGCAA GATCCCAGAG TGAGAGGCCT GTATCTCCCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGTTCCGA CTACTGTCTC TCCCATATCG	120
TCAATCTTCT CGAGGATTGG GGACCGCTGCG CTGAACATGG AGAACATCAC ATCAGGATT	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCGAAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTTC TAGGGGAAAC CACCGTGTGT	300
CTTGGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCA ACT	360
TGTCCCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTATCA TCTTCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGTG GGTTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCT	480
CTGATTCCAG GATCTTCAAC CACCAGCACG GGACCATGCA GAACCTGCAC GACTCCTGCT	540
CAAGGAACCT CTATGTATCC CTCCTGTTGC TGTACCAAAC CTTGGACGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTT ACTAGTGCCA TTTGTTCAAGT GGTTGTTAGG GCTTTCCCCC	720

ACTGTTGGC TTTAGTTAT ATGGATGATG TGGTATTGGG GGCCAAA ACT GTTCACCAC	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATCTAAAC	840
CTAACAAAAC AAAAAGATGG GGTTACTCTT TACATTTAT GGGCTATGTC ATTGGATGTT	900
ATGGGTCTTT GCCACAAGAT CACATCATA AGAAAATCAA AGAATGTTT AGAAAAC	960
CTGTTAACAG GCCTATTGAT TGGAAAGTCT GTCAACGTAT TGTGGTCTT TTGGGATTG	1020
CTGCTCTTT TACACAATGT GGTTATCCTG CTTTAATGCC CTTGTATGCA TGTATTCAAT	1080
CTAACGCAGGC TTTCACTTTC TCGCCAAC TT ACAAGGCCTT TCTGTGTAAA CAATAC	1140
ACCTTTACCC CGTTGCCCGG CAACGCCAG GTCTGTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGTC ATGGGCCATC AGCGCATGCG TGGAACCTTT CAGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTGC TCGCAGCCGG TCTGGAGCAA	1320
ACATTCTCGG GACGGATAAC TCTGTTGTC TCTCCCGCAA ATATACTCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTGTTAC GTCCCCTCGG	1440
CGCTGAATCC CGCGGACGAC CCTTCTCGGG GCCGCTTGGG ACTCTCTCGT CCCCTCTCC	1500
GTCTGCCGTT TCGACCGACC ACGGGGCGCA CCTCTCTTTA CGCGGACTCC CGCTCTGTGC	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTCACCTCT GCACGTGCA TGGAGACCAC	1620
CGTGAACGCC CACCAATTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCTGT	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAGG ACTGGGAGGA	1740
GTCGGGGGAG GAGATTAGAT TAATGATCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTCAC CTCTGCCAA TCATCTCTTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTCTAGG ACATGGACAT TGATCCTTAT	1920
AAAGAATTG GAGCTACTGT GGAGTTACTC TCGTTCTGC CTTCTGACTT CTTTCCTTCA	1980
GTACGAGATC TTCTAGATAC CGCCTCAGCT CTATATCGGG AAGCCTTAGA ATCTCCTGAG	2040
CATTGTTCAC CTCACCATAAC TGCACTCAGG CAAGCAATT TCTGCTGGGG GGATCTAATA	2100
ACTCTATCCA CCTGGGTGGG TGGTAATTG GAAGATCCAA CATCTAGGGA CCTAGTAGTC	2160
AGTTATGTTA ACACTAATAT GGGCTAAAG TTCAGGCAAC TATTGTGGTT TCACATTCT	2220
TGTCTCACTT TTGGAAGAGA AACGGTCATA GAGTATTTGG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAGACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCACGTG CAGAAGAACT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
CTGGACTCAT AAGGTGGGAA ACTTACGGG GCTTTATTCT TCTACTGTC CTGTCTTTAA	2520
CCCTCATTGG AAAACACCCCT CTTTCCTAA TATACATTAA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAA TTTGTAGGCC CACTCACAGT CAATGAGAAA AGAAGACTGC AATTGATTAT	2640
GCCTGCTAGG TTTTATCCAA AGGTTACCAA ATATTGCCA TTGGATAAGG GTATTAAACC	2700

TTATTATCCA	GAACATCTAG	TTAATCATTA	CTTCCAAACC	AGACATTATT	TACACACTCT	2760
ATGGAAGGCG	GGTGTATTAT	ATAAGAGAGA	AACTACACAT	AGCGCCTCAT	TTTGTGGTC	2820
ACCATATTCC	TGGGAACAAG	AGCTACAGCA	TGGGGCAGAA	TCTTCCACC	AGCAATCCTC	2880
TGGGATTCTT	TCCCCGACAC	CAGTTGGATC	CAGCCTTCAG	AGCAAACACT	GCAAATCCAG	2940
ATTGGGACTT	CAATCCCAAC	AAGGACTCCT	GGCCAGACGC	CAACAAGGT	GGAGCTGGAG	3000
CATTGGGCT	GGGATTCAAC	CCACCGCACG	GAGGCCTTTT	GGGGTGGAGC	CCTCAGGCTC	3060
AGGGCATACT	ACAAACCTTG	CCAGCAAATC	CGCCTCCTGC	CTCCACCAAT	CGCCAGTCAG	3120
GAAGGCAACC	TACCCCTCTG	TCTCCACCTT	TGAGAAACAC	TCATCCTCAG	GCCATGCAGT	3180
GG						3182

(2) INFORMATION FOR SEQ ID NO: 307:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3182 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO
- (iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 307:

AACTCCACAA	CCTTCCACCA	AACTCTGCAA	GATCCCAGAG	TGAGAGGCCT	GTATTTCCCT	60
GCTGGTGGCT	CCAGTTCAAG	AACAGTAAAC	CCTGTTCCGA	CTACTGTCTC	TCCCATATCG	120
TCAATCTTCT	CGAGGATTGG	GGACCCTGCG	CTGAACATGG	AGAACATCAC	ATCAGGATTG	180
CTAGGACCCC	TGCTCGTGT	ACAGGGGGGG	TTTTCTTGT	TGACAAGAAT	CCTCACAATA	240
CCGCAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGAAC	TACCGTGTGT	300
CTTGGCCAAA	ATTCGCAGTC	CCCAACCTCC	AATCACTCAC	CAACCTCCTG	TCCTCCAAC	360
TGTCCCTGGTT	ATCGCTGGAT	GTGTCTGCGG	CGTTTTATCA	TCTTCCTCTT	CATCCTGCTG	420
CTATGCCCTCA	TCTTCTTGT	GGTTCTCTG	GACTATCAAG	GTATGTTGCC	CGTTTGTCC	480
CTAATTCCAG	GATCTTCAAC	TACCAAGCACG	GGACCATGCA	GAACCTGCAC	GAACCTGCT	540
CAAGGAACCT	CTATGTATCC	CTCCTGTTGC	TGTACCAAAC	CTTCGGACGG	AAATTGCACC	600
TGTATTCCCA	TCCCCATCATC	CTGGGCTTTC	GGAAAATTCC	TATGGGAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCCA	TTTGTTCAGT	GGTTCGTAGG	GCTTCCCC	720
ACTGTTGGC	TTTCAGTTAT	ATGGATGATG	TGGTATTGGG	GGCCAAGTCT	GTACAGCATC	780
TTGAGTCCCT	TTTTACCGCT	GTTACCAATT	TTCTTCTGTC	TTTGGGTATA	CATTTAAACC	840
CTAACAAAAC	AAAAAGATGG	GGTTACTCTT	TACATTCAT	GGGCTATGTC	ATTGGATGTT	900

ATGGGTCA	T GCCACAAGAT CACATCATA	C AGAAAATCAA AGAATGCTT	AGAAAAC	TC 960
CTGTTAACAG	GCCTATTGAT TGGAAAGTCT GTCAACGTAT	TGTGGTCTT TTGGGTTTG		1020
CTGCCCTT	TACACAATGT GGTTATCCTG CTTTAATGCC	TTTGTATGCA TGTATTCA	GT 1080	
CGAACAGGC	TTTTACTTTC TCGCCAAC	TT ACAAGGCCTT TCTGTGTAAA CAATAC	CTGA 1140	
ACCTTACCC	CGTTGCCCGG CAACGGCCAG GTCTGTGCCA	AGTGTGCT GACGCAAC	CC 1200	
CCACTGGCTG	GGGCTTGTC ATGGGCCATC AGCGCATGCG	TGGAACCTT CTGGCTCGTC	1260	
TGCCGATCCA	TACTGCGAA CTCCTAGCCG CTTGTTTGC	TCGCAGCAGG TCTGGAGCAA	1320	
ACATTCTCGG	GACGGATAAC TCTGTTGTC TCTCCCGCAA	ATATACATCG TATCCATGGC	1380	
TGCTAGGCTG	TGCTGCCAAC TGGATCCTGC GCGGGACGTC	CTTTGTTAC GTCCCCTCGG	1440	
CGCTGAATCC	CGCGGACGAC CCTTCTCGGG GTCGCTTGGG	ACTCTCTCGT CCCCTCTCC	1500	
GTCTGCCGTT	TCGACCGACC ACGGGGCGCA CCTCTCTTTA	CGCGGACTCC CCGTCTGTGC	1560	
CTTCTCATCT	GCCGGACCGT GTGCACTTCG CTTCACCTCT	GCACGTGCA TGGAGACCAC	1620	
CGTGAAAGCC	CAACCATTCT TGCCCAAGGT CTTACATAAG	AGGACTCTTG GACTCTCTGT	1680	
AATGTCAACG	ACCGACCTTG AGGCATACTT CAAAGACTGT	TTGTTAAAG ACTGGGAGGA	1740	
GTTGGGGGAG	GAGATTAGAT TAAAGGTCTT TGTATTAGGA	GGCTGTAGGC ATAAATTGGT	1800	
CTGCGCACCA	GCACCATGCA ACTTTTCAC CTCTGCCAA	TCATCTCTTG TTCATGTCC	1860	
ACTGTTCAAG	CCTCCAAGCT GTGCCTTGGG TGGCTTGGG	GCATGGACAT TGATCCTTAT	1920	
AAAGAATTG	GAGCTACTGT GGAGTTACTC TCGTTTTGC	CTTCTGACTT CTTCCCTTCA	1980	
GTACGAGATC	TTCTAGATAA CGCCTCAGCT CTGTATCGGG	AAGCCTTAGA GTCTCCTGAG	2040	
CATTGTTCAC	CTCACCAATAC TGCACTCAGG CAAGCAATAC	TGTGCTGGGG GGAACATAATG	2100	
ACTCTAGCTA	CCTGGGTGGG TGGTAATTG GAAGATCAA	TATCCAGGG CCTAGTAGTC	2160	
AGTTATGTCA	ACACTAATAT GGGCCTAAAA TTCAGGCAAC	TATTGTGGTT TCACATTCT	2220	
TGTCTCACTT	TTGGAAGAGA AACAGTTATA GAGTATTGG	TGTCTTTGG AGTGTGGATT	2280	
CGCACTCCTC	CAGCTTATAG ACCACCAAAT GCCCCTATCT	TATCAACACT TCCGGAGACT	2340	
ACTGTTGTTA	GACGACGAGG CAGGTCCCC	AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400	
AGGTCTCAAT	CGCCGCGTCG CAGAAGATCT CAATCTCGGG	AATCTCAATG TTAGTATTCC	2460	
TTGGACTCAT	AAGGTGGGAA ACTTTACGGG GCTTTATTCT	TCTACTGTAC CTGTCTTAA	2520	
CCCTCATTGG	AAAACACCCCT CTTTCCTAA TATACATTAA	CACCAAGACA TTATCAAAAA	2580	
ATGTGAACAA	TTTGTAGGCC CACTCACAGT CAATGAGAAA	AGAAGACTGC AATTGATTAT	2640	
GCCAGCTAGG	TTTTATCCAA ATGTTACCAA ATATTTGCCA	TTGGATAAGG GTATTAAACC	2700	
TTATTATCCA	GAATATTAG TTAATCATTA CTTCCAAACT	AGACATTATT TACACACTCT	2760	
ATGGAAGGCG	GGTATATTAT ACAAGAGAGA AACTACACAT	AGCGCCTCAT TTTGTGGGTC	2820	
ACCATATTCT	TGGGAACAAG AGCTACAGCA TGGGGCAGAA	TCTTTCCACC AGCAATCCTC	2880	

TGGGATTCTT TCCCGACCAAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000
CATTCGGGCT GGGATTCAACC CCACCACACG GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATACT AGAAACGTTG CCAGCAAATC CGCCTCCTGC CTCTACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCCGCTG TCTCCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 308:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3182 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 308:

AACTCCACAA CTTTCCACCA AACTCTGCAA GATCCCAGGG TGAGAGGGCT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAAG AACAGTAAAC CCTGTTCCGA CTACTGCCTC TCCCATATCG	120
TCAATCTTCT CGAGGATTGG GGACCCCTGCA CTGAACATGG AGAACATCAC ATCAGGATTC	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAGAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGAAC CACCGTGTGT	300
CTTGGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCCTG TCCTCCA ACT	360
TGTCTGGTT ATCGCTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTT	420
CTATGCCTCA TCTTCTTGTGTT GGTTCTACTG GACTATCAAG GTATGTTGCC CGTGTGTCT	480
CTAATTCCAG GATCTTCAAC CACCAGCGCG GGACCATGCA GAAACCTGCAC GACTACTGCT	540
CAAGGAACCT CTATGTATCC CTCCCTGTTGC TGTACCAAAC CTTCGGACGG AAATTGCACC	600
TGTATTCCCA TCCCATCATC CTGGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCAAGT GGTTCGTAGG GCTTTCCCCC	720
ACTGTTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACAGCATE	780
TTGAGTCCCT TTTTACCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAACC	840
CTAACAAAAC TAAGAGATGG GGTTACCTTT TACATTCAAT GGGCTATGTC ATTGGAAGTT	900
ATGGGTCAATT GCCACAAGAT CACATCATAAC AGAAAATCAA AGAATGTTT AGAAAACCTTC	960
CTATTAACAG GCCTATTGAT TGGAAAGTCT GTCAACGTAT TGTGGGTCTT TTGGGTTTG	1020

CTGCCCTTT TACACAATGT GGTTATCCTG CTTTAATGCC CTTGTATGCC TGTATTCAAT	1080
CTAAACAGGC TTTCACTTTC TCGCCAACCT ACAAGGCCCT TCTGTGTAAA CAATACCTGA	1140
ACCTTACCC CGTTGCTAGG CAACGGCCAG GTCTGTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGTC ATGGGCCATC AGCGCATGCG TGGAACCTTT CTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTAGCCG CTTGTTTGC TCGCAGCAGG TCTGGAGCAA	1320
ACATTCTCGG GACGGATAAC TCTGTTGTT CTCCTCCGAA ATATACATCG TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTGTTTAC GTCCCGTCGG	1440
CGCTGAATCC CGCGGACGAC CCTCTCTCGGG GCCGCTTGGG GATCTTCGT CCCCTCTCC	1500
GTCTGCCGTT CCGTCCGACC ACGGGGCGCA CCTCTCTTA CGCGGACTCC CCGTCTGTGC	1560
CTTCTCATCT GCCGGTCCGT GTGCACTTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCACTTCT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCAGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTTAAGG ACTGGGAGGA	1740
GTTGGGGAG GAGATTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCTTG TTCATGTCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCCTAT	1920
AAAGAATTG GAGCTACTGT GGAGTTACTC TCATTTTGC CTTCTGACTT TTTCCCTTCG	1980
GTACGAGATC TTCTAGATAAC CGCCTCAGCT CTGTATCGGG ATGCCTTAGA GTCTCCTGAG	2040
CATTGTTCAC CTCACCATAAC TGCACTCAGG CAAGCAATTCAAGCTGGG GGAACTAATG	2100
ACTCTAGCTA CCTGGGTGGG TGTAAATTG GAAGATCCAG CATCTAGGGA CCTAGTAGTC	2160
AGTTATGTCA ACACATAATAT GGGCCTAAAG TTCAGGCAAC TATTGTGGTT TCACATTCT	2220
TGTCTCACTT TTGGAAGAGA AACAGTCATA GAGTATTGG TGTCTTTCGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGATCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCGGG AATCTCAATG TTAGTATTCC	2460
TTGGACTCAT AAAGTGGGTA ACTTTACGGG GCTTTATTCC TCTACTGTAC CTGTCTTAA	2520
CCCTCATTGG AAAACACCCCT CTTTCCTAA TATACATCTA CACCAAGACA TTATCAAAAA	2580
ATGTGAACAA TTTGTAGGCC CACTCACAGT AAATGAGAAA CGAAGACTGC AATTAATTAT	2640
GCCTGCTAGG TTTTATCCAA ATGTTACTAA ATATTTGCCA TTAGATAAGG GTATTAAACC	2700
TTATTATCCG GAACATTTAG TTAATCATTAA CTTCCAAACC AGACATTATT TACACACTCT	2760
ATGGAAGGCG GGTATATTAT ATAAGAGGGAA AACAAACACGT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGGCAGAA TCTTCCACC AGCAATCCTC	2880
TGGGATTCTT TCCCGACCAC CAGTTGGATC CAGCCTTCAG AGCAAACACC GCAAATCCAG	2940
ATTGGGACTT CAATCCCAAC AAGGACACCT GGCCAGACGC CAACAAGGTA GGAGCTGGAG	3000

CATTGGGCT GGGATTCA CCACCGCACG GAGGCCTTT GGGGTGGAGC CCTCAGGCTC	3060
AGGGCATAAT ACAAACCTTG CCAGCAAATC CGCCTCCTGC ATCTACCAAT CGCCAGTCAG	3120
GAAGGCAGCC TACCCCGCTG TCTCACCTT TGAGAAACAC TCATCCTCAG GCCATGCAGT	3180
GG	3182

(2) INFORMATION FOR SEQ ID NO: 309:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3212 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 309:

AACTCCACAA CATTTCATCA AGCTCTGCAG GATCCCAGAG TAAGAGGCCT GTATTTCT	60
GCTGGTGGCT CCAGTTCCGG AACAGTGAAC CCTGTTCCGA CTACTGCCTC ACTCATCTCG	120
TCAATCTTCT CGAGGATTGG GGACCTGCA CCGAACATGG AAAGCATCAC ATCAGGATT	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTTCTTGT TGACAAAAAT CCTCACAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC TCCC GTGTGT	300
CTTGGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCCTGGCT ATCGCTGGAT GTGCTCTGCC CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTCTG GACTATCAAG GTATGTTGCC CGTTGTCT	480
CTAATTCCAG GATCATCAAC CACCAGCACG GGACCCCTGCC GAACCTGCAT GACTCTTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTTCAAAAC CTTGGACGG AAATTGCACT	600
TGTATTCCCA TCCCATCATC ATGGGCTTTC GGAAAATTCC TATGGGAGTG GGCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCAAGT GGTTGCCGG GCTTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAGTCT GTACGACATC	780
TTGAGTCCCT TTATACCTCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAATC	840
CCAACAAAAC AAAAAGATGG GGATATTCCC TAAATTCAT GGGTTATGTA ATTGGAAAGTT	900
GGGGGTCATT ACCACAGGAA CACATCATAAC AAAAATCAA ACACTGTTT GGAAACTCC	960
CTGTTAACCG GCCTATTGAT TGGAAAGTAT GTCAAGGAAT TGTGGTCTT TTGGGCTTTG	1020
CTGCCCTTT TACACAATGT GGGTATCCTG CTTTAATGCC TCTGTATAACG TGTATTCAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACCTT ACAAGGCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCCGG CAACGGCCAG GTCTGTGCCA AGTGTGCT GATGCAACCC	1200

CCACTGGCTG	GGGCTTGGCC	ATAGGCATTC	AGCGCATGCG	CGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCCG	CTTGGTTTGCG	TCGCAGCAGG	TCTGGAGCAA	1320
AACTTATCGG	GACCGATAAT	TCTGTCGTTTC	TCTCCCGGAA	ATATACATCC	TTTCCATGGC	1380
TGCTAGGCTG	TGCTGCCAAC	TGGATCCTGC	GAGGGACGTC	CTTTGTCTAC	GTCCC GTCA	1440
CGCTGAATCC	TGCGGACGAC	CCGTC TCGGG	GTCGCTTGGG	GATCTTCGT	CCCCTCTCC	1500
GTCTGCGGTT	CCGGCCGACC	ACGGGGCGCA	CCTCTCTTA	CGCGGTCTCC	CCGTCTGTGC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTCGCA	TGGAGACCAC	1620
CGTGAACGCC	CACCAAATCT	TGCCCAAGGT	CTTACATAAG	AGGACTCTTG	GACTCTCTGC	1680
AATGTCAACG	ACCGACCTTG	AGGCATACTT	CAAAGACTGT	TTGTTAAAG	ACTGGGAGGA	1740
GTTGGGGAG	GAGATTAGAT	TAAAGGTCTT	TGTACTAGGA	GGCTGTAGGC	ATAAATTGGT	1800
CTGCGCACCA	GCACCATGCA	ACTTTTCAC	CTCTGCCTAA	TCATCTCTTG	TTCATGTCCT	1860
ACTGTTCAAG	CCTCCAAGCT	GTGCCTTGGG	TGGCTTGGG	GCATGGACAT	TGACCCTTAT	1920
AAAGAATTG	GAGCTACTGT	GGAGTTACTC	TCGTTTTGC	CTTCTGACTT	CTTCCTTCA	1980
GTAAGAGATC	TTCTAGATAAC	CGCCTCAGCT	CTGTATCGGG	ATGCCTTAGA	ATCTCCTGAA	2040
CATTGTTCAC	CGCACCAACAC	TGCACTCAGG	CAAGCCATT	TTTGCTGGGG	GGAACTAATG	2100
ACTCTAGCTA	CCTGGGTGGG	TGTAAATTG	GAAGATCCAG	CATCCAGGG	CCTAGTAGTC	2160
AGTTATGTCA	ATACTAATAT	GGGCCTAAAG	TTCAGGCAAT	TATTGTGGTT	TCACATTCT	2220
TGTCTCACTT	TTGGAAGAGA	AACCGTCATA	GAGTATTGG	TGTCTTTGG	AGTGTGGATT	2280
CGCACTCCTC	CAGCTTATAG	ACCACCAAAT	GCCCCTATCT	TATCAACACT	TCCGGAGAAT	2340
ACTGTTGTTA	GACGAAGAGG	CAGGTCCCC	AGAAGAAGAA	CTCCCTCGCC	TCGCAGACGA	2400
AGATCTCAAT	CGCCGCGTCG	CAGAAGATCT	CAATCTCCAG	CTTCCAATG	TTAGTATTCC	2460
TTGGACTCAT	AAGGTGGGAA	ATTTACGGG	GCTCTACTCT	TCTACTATT	CTGTCTTTAA	2520
TCCTAACTGG	AAAACCTCCAT	CTTTCTGA	TATTCAATTG	CACCAGGACA	TTATTAACAA	2580
ATGTGAACAA	TTTGTAGGTC	CTCTAACAGT	AAATGAAAAA	CGAAGATTAA	ACTTAGTCAT	2640
GCCTGCTAGA	TTTTTCCCA	TCTCTACAAA	ATATTGCC	CTAGAGAAAG	GTATAAAACC	2700
TTATTATCCA	GATAATGTAG	TTAATCATT	CTTCCAAACC	AGACACTATT	TACATACCC	2760
ATGGAAGGCT	GGGCATCTAT	ATAAAAGAGA	AACTACACGT	AGCGCTCAT	TTTGTGGGTC	2820
ACCATATTCT	TGGGAACAAG	AGCTACATCA	TGGGGCTTTC	TTGGACGGTC	CCTCTCGAAT	2880
GGGGGAAGAA	TATTTCACC	ACCAATCCTC	TGGGATTTT	TCCCGACCAC	CAGTTGGATC	2940
CAGCATTCA	AGCAAACACC	AGAAATCCAG	ATTGGGACCA	CAATCCAAC	AAAGACCACT	3000
GGACGGAAGC	CAACAAGGTA	GGAGTGGGAG	CCTTCGGGCC	GGGGTTCACT	CCCCCACACG	3060
GAGGCCTTT	GGGGTGGAGC	CCTCAGGCTC	AAGGCATGCT	AAAAACATTG	CCAGCAGACC	3120
CGCCTCCTGC	CTCCACCAAT	CGGCAGTCAG	GAAGGCAGCC	TACCCCAATC	ACTCCACCTT	3180

TGAGAGACAC TCATCCTAG GCCATGCA GT GG

3212

(2) INFORMATION FOR SEQ ID NO: 310:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3212 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 310:

AATTCCACAA CATTCCACCA AGCTCTGCAG GATCCCAGAG TAAGAGGCCT GTATTTCC	60
GCTGGTGGCT CCAGTTCCGG AACAGTGAAC CCTGTTCCGA CTACTGCCTC ACTCATCTCG	120
TCAATCTTCT CGAGGATTGG GGACCCTGCA CCGAACATGG AAAGCATCAC ATCAGGATT	180
CTAGGACCCC TGCTCGTGT ACAGGCGGGG TTTTCTTGT TGACAAAAAT CCTCACAAATA	240
CCGCAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGAGC TCCCGTGTGT	300
CTTGGCCAAA ATTCCGAGTC CCCAACCTCC AGTCACTCAC CAACCTCTTG TCCTCCAATT	360
TGTCCCTGGCT ATCGCTGGAT GTGTCTGCCG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCTCA TCTTCTTGT GGTTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCT	480
CTAATTCCAG GATCATCAAC CACCACTACG GGACCCTGCC GAACCTGCAC GACTCTTGCT	540
CAAGGAACCT CTATGTTCC CTCATGTTGC TGTTCAAAAC CTTGGACGG AAATTGCACT	600
TGTATTCCCA TCCCCATCATC ATGGCTTTC GGAAAATTCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCCA TTTGTTCACT GGTTGCCGG GCTTCCCCC	720
ACTGTCTGGC TTTCAGTTAT ATGGATGATG TGGTATTGGG GGCCAAAGTCT GTACAACATC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTTTGTC TTTGGGTATA CATTAAATC	840
CCAACAAAAAC AAAAAGATGG GGCTATTCCC TTAATTTCAT GGGTTATGTA ATTGGAAGTT	900
GGGGCTCATT ACCACAGGAA CACATCATAAC AAAAATCAA AGACTGTTT AGAAAACCTCC	960
CTGTTAACCG GCCTATTGAT TGGAAAGTAT GTCAAAGAAT TGTGGGTCTT TTGGGCTTTG	1020
CTGCCCTT TACACAATGT GGATATCCTG CTTTAATGCC TCTGTATGCA TGTACTCAAT	1080
CTAAGCAGGC TTTCACTTTC TCGCCAACCTT ACAAGGCCTT TCTGTGTAAA CAATACCTGA	1140
ACCTTTACCC CGTTGCCGG CAACGGCCAG GTCTGTGCCA AGTGTGTTGCT GATGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATAGGCATTC AGCGCATGCG CGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCCTAGCCG CTTGTTTGC TCGCAGCAGG TCTGGAGCAA	1320

AACTTATCGG GACCGATAAT TCTGTCGTT C TCTCCGGAA GTATA CATCC TTTCCATGGC	1380
TGCTAGGCTG TGCTGCCAAC TGGATCCTGC GAGGGACGTC CTTTGTCTAC GTCCCCTCAG	1440
CGCTGAATCC TGCGGACGAC CCGTCTCGGG GTCGCTTGGG GATCTATCGT CCCCTCTCC	1500
GTCTGCCGT CCAGCCGACC ACGGGGCGCA CCTCTCTTA CGCGGTCTCC CCGTCTGTT	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CACCAAATAT TGCCCAAGGT CTTACATAAG AGGACTCTTG GACTCTCTGC	1680
AATGTCAACG ACCGACCTTG AGGCATACTT CAAAGACTGT TTGTTAAAG ACTGGGAGGA	1740
GTCGGGGAG GAGATTAGAT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCTTG TTCATGTCCT	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTTGGG GCATGGACAT TGACCCCTAT	1920
AAAGAATTG GAGCTACTGT GGAGTTACTC TCGTTTTGC CTTCTGACTT CTTTCCTTCA	1980
GTAAGAGATC TTCTAGATAAC CGCCTCAGCT CTGTATCGGG ATGCCTTAGA GTCTCCTGAG	2040
CATTGTTCAC CTCACCACAC TGCACTCAGG CAAGCCATTG TTTGCTGGGG AGAACTAATG	2100
ACTCTAGCTA CCTGGGTGGG TGTAAATTG GAAGATCCAG CATCCAGGGG CCTAGTAGTC	2160
AGTTATGTCA ATACTAATAT GGGCCTAAAG TTCAGGCAAT TATTGTGGTT TCACATTCT	2220
TGTCTCACTT TTGGAAGAGA AACCGTCATA GAGTATTG TGTCTTTGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCTATCT TATCAACACT TCCGGAGAAT	2340
ACTGTTGTTA GACGAAGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGATCTCAAT CGCCCGCTCG CAGAAGATCT CAATCTCCAG CTTCCCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGAA ATTTTACGGG GCTTTACTCT TCTACTATAC CTGTCTTTAA	2520
TCCCTAACTGG AAAACTCCAT CTTTCCTGA TATTCAATTG CACCAGGACA TTATTAACAA	2580
ATGTGAACAA TTTGTAGGTC CTCTAACTGT AAATGAAAAA CGAAGATTAA ACTTAGTCAT	2640
GCCTGCTAGA TTTTTCCCA TCTCTACGAA ATATTTGCCCTAGAGAAAG GTATAAAACC	2700
TTATTATCCA GATAATGTAG TTAATCATTAA CTTCCAAACC AGACACTATT TACATACCCT	2760
ATGGAAGGCG GGCATCTTAT ATAAAAGAGA AACTACACGT AGCGCCTCAT TTTGTGGGTC	2820
ACCTTATTCT TGGGAACAAG AGCTACATCA TGGGGCTTTC TTGGACGGTC CCTCTCGAAT	2880
GGGGGAAGAA TATTTCACC ACCAATCCTC TGGGATTTTT TCCCGACCAC CAGTTGGATC	2940
CAGCATTCAAG AGCAAACACC AGAAATCCAG ATTGGGACCA CAATCCAAC AAAGACCACT	3000
GGACAGAAGC CAACAAGGTA GGAGTGGGAG CATTGGGCC TGGGTTCACT CCCCCACACG	3060
GAGGCCTTTT GGGGTGGAGC CCTCAGGCTC AAGGCATGCT AAAAACATTG CCAGCAGATC	3120
CGCCTCCTGC CTCCACCAAT CGGCAGTCAG GAAGGCAGCC TACCCCAATC ACTCCACCTT	3180
TGAGAGACAC TCATCCTCAG GCCATGCAGT GG	3212

(2) INFORMATION FOR SEQ ID NO: 311:

(i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 3215 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 311:

AACTCAACTC ACTTCCACCA AGCTCTGTTG GATCCCAGGG TAAGGGCACT GTATTTCCCT	60
GCTGGTGGCT CCAGTTCAAGG AACACAGAAC CCTGCTCCGA CTATTGCCTC TCTCACATCA	120
TCAATCTCCT CGAAGACTGG GGGCCCTGCT ATGAACATGG AGAACATCAC ATCAGGACTC	180
CTAGGACCCC TGGCGGTGTT ACAGGCGGTG TGTTTCTTGT TGACAAAAAT CCTCACAAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGACT ACCCAGGTGT	300
CCTGGCCAAA ATT CGCAGTC CCCAACCTCC AATCACTTAC CAACCTCCTG TCCTCCA ACT	360
TGTCCCTGGCT ATCGTTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGTG GGTCTTCTG GACTACCAAG GTATGTTGCC CGTTTGTCC	480
CTACTTCCAG GATCCACGAC CACCAGCACG GGACCATGCA AAACCTGCAC AGCTCTTGCT	540
CAAGGAACCT CTATGTTCC CTCCTGTTGC TGTTCCAAAAC CCTCGGACGG AACTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTA GGAAAATACC TATGGGAGTG GGCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCAA TTTGTTCACT GGTGCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTTAGTTAT ATGGATGATC TGGTATTGGG GGCCAAATCT GTGCAGCATC	780
TTGAGTCCTT TTATACCGCT GTTACCAATT TTCTGTTATC TGTGGGTATC CATTAAATA	840
CTGCTAAAAC AAAAAGATGG GGTTACAACC TACATTTCAT GGGTTATGTT ATTGGTAGTT	900
GGGGAACGTT ACCCCAAGAT CATATTGTAC ACAAAATCAA AGATTGTTT CGAAAAGTTC	960
CTGTAAATCG CCCAATTGAT TGGAAAGTTT GTCAAAGTAT TGTGGGTCTT TTGGGCTTTG	1020
CGGCCCCCTT TACCCAATGT GGTTATCCTG CTCTCATGCC TTTGTATGCC TGTATTACTG	1080
CTAAACAGGC TTTTGTCTTC TCGCCAACCT ACAAGGCCTT TCTGTGTAAA CAATACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGCCAG GCCTGTGCCA AGTGTGTTGCT GACGCAACCC	1200
CCACTGGCTG GGGCTTGGCC ATAGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCTTGCAG CTTGCTTCGC TCGCAGCCGG TCTGGAGCAA	1320
TCCTCATCGG CACAGACAAT TCTGTCGTCC TCTCTCGGAA GTATACATCC TTTCCATGGC	1380
TGCTCGGTTG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTGTTAC GTCCCGTCGG	1440
CGCTGAATCC AGCGGACGAA CCCTCCCGGG GTCGCTTGGG GCTGTACCGC CCCCTTCTTC	1500

GTCTGCCGTT CCAGCCGACA ACGGGTCGCA CCTCTCTTA CGCGGACTCC CCGTCTGTT	1560
CTTCTCATCT GCCGGACCGT GTGCACTTCG CTTCACCTCT GCACGTCGCA TGGAGACCAC	1620
CGTGAACGCC CCCTGGAGTT TGCCAACAGT CTTACATAAG AGGACTCTTG GACTTCAGG	1680
ACGGTCAATG ACCTGGATCG AAGACTACAT CAAAGACTGT GTATTTAAGG ACTGGGAGGA	1740
GCTGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTCTTG TTCATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCTTAT	1920
AAAGAATTG GAGCTCTGT GGAATTGTT TCCTTTTGG CTTCTGACTT CTTTCCGTCT	1980
GTTCGGGACC TCCTCGACAC CGCCTCAGCC CTGTACCGGG ATGCCTTAGA GTCACCGGAA	2040
CATTGCACCC CCAATCATAAC CGCTCTCAGG CAAGCTATTT TGTGCTGGGG TGAGTTAATG	2100
ACTTTGGCTT CCTGGGTGGG TAATAATTG GAAGACCTG CAGCTAGGGA TTTAGTAGTT	2160
AATTATGTCA ACACTAATAT GGGCTTAAAG ATTAGACAAC TATTGTGGTT TCACATCTCC	2220
TGTCTTACTT TTGGAAGAGA AACAGTTCTT GAGTATTG TGTCCTTGG AGTGTGGATT	2280
CGCACTCCAC CTGCTTATAG ACCACCAAAT GCCCCTATCC TATCCACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCGCC TCGCCGACGA	2400
AGGTCTCAAT CGCCGGCTCG CAGAAGATCT CAATCTCCAG CTTCCCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGAA ATTTTACGGG GCTCTACTCT TCTACTGTAC CTGCTTCAA	2520
TCCTAACTGG TTAACCTCTT CTTTCCTGA TATTCAATTAA CATCAGGATA TGATATCTAA	2580
ATGTGAACAA TTTGTAGGCC CGCTCACTAA AAATGAATTG AGAAGATTAA AATTGGTCAT	2640
GCCAGCTAGA TTTTATCCTA AGCATAACCA AAATTCCTA TTGGAGAAAG GGATTAACCC	2700
CTATTATCCA GATCAGGCAG TTAATCATTA TTTCAAACCC AGACATTATT TGCATACTTT	2760
ATGGAAGGCG GGAATTCTAT ATAAGAGAGA AACCAACACGT AGCGCCTCAT TTTGTGGTC	2820
ACAATATTCC TGGGAACAAG AGCTACAGCA TGGGAGCACC TCTCTCAACG ACAAGAAGGG	2880
GCATGGGACA GAATCTTCT GTGCCCAATC CACTGGCTT CTTGCCAGAC CATCAGCTGG	2940
ATCCGCTATT CAGAGCAAAT TCCAGCAGTC CCGACTGGGA CTTCAACACA AACAGGACA	3000
GTTGGCCAAT GGCAAACAAG GTAGGAGTGG GAGGCTACGG TCCAGGGTTC ACACCCCCAC	3060
ACGGTGGCCT GCTGGGTGG AGCCCTCAGG CACAGGGTGT TTTAACAAACC TTGCCAGCAG	3120
ATCCGCTCC TGCTTCCACC AATCGGCTGT CCGGGAGGAA GCCAACCCAA GTCTCTCCAC	3180
CTCTAAGAGA CACACATCCT CAGGCCATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 312:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 3215 base pairs
  - (B) TYPE: nucleic acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 312:

AACTCAACTC ACTTCCACCA GGCTCTGTTG GATCCGAGGG TAAGGGCACT GTATTTCCCT	60
GCTGGTGGCT CCAGTCAGG CACGCAGAAC CCTGCTCCGA CTATTGCCTC TCTCACATCA	120
TCAATCTCCT CGAAGACTGG GGGCCCTGCT ATGAACATGG ACAACATCAC ATCAGGACTC	180
CTAGGACCCC TGCTCGTGT ACAGGCCTG TGTTCTTGT TGACAAAAAT CCTCACAATA	240
CCACAGAGTC TAGACTCGTG GTGGACTTCT CTCAATTTC TAGGGGGACT ACCCGGGTGT	300
CCTGGCCAAA ATTCCGAGTC CCCAACCTCC AATCACTTAC CAACCTCCTG TCCTCCAATC	360
TGTCCTGGCT ATCGTTGGAT GTGTCTGCGG CGTTTTATCA TCTTCCTCTT CATCCTGCTG	420
CTATGCCCTCA TCTTCTTGTGTT GGTTCTTCTG GACTATCAAG GTATGTTGCC CGTTTGTCT	480
CTAATTCCAG GATCTACGAC CACCAGCAGC GGACCATGCA AAACCTGCAC AACTCTGCT	540
CAAGGAACCT CTATGTTCC CTCCTGTTGC TGTTCCAAAC CCTCGGACGG AAACCTGCACC	600
TGTATTCCCA TCCCATCATC TTGGGCTTTA GGAAATACCC TATGGGAGTG GGCCTCAGCC	660
CGTTTCTCCT GGCTCAGTTT ACTAGTGCAA TTTGTTCACT GGTGCGTAGG GCTTTCCCCC	720
ACTGTCTGGC TTTTAGTTAT ATGGATGATC TGGTATTGGG AGCCAAATCT GTGCAGCCTC	780
TTGAGTCCCT TTATACCGCT GTTACCAATT TTCTGTTATC TGTGGGTATC CATTGAAATA	840
CCTCTAAAAC AAAAAGATGG GGTTACAATT TACATTCAT GGGTTATGTC ATTGGCAGTT	900
GGGGAGCATT ACCCCAAGAT CATATTGTAC ACAAAATCAA AGAATGTTTT CGAAAAGTTC	960
CTGTAAATCG TCCAATTGAC TGGAAAGTTT GTCAACGTAT TGTGGGACTT TTGGGCTTTG	1020
CTGCTCCTTT TACCCAAATGT GGTTATGCTG CTCTCATGCC TCTGTATAAC TGTATCACTG	1080
CGAAACAGGC TTTTGTCTTT TCGCCAACCTT ACAAGGCCTT TCTCTGTAAA CAGTACATGA	1140
ACCTTTACCC CGTTGCTCGG CAACGGCCAG GCCTGTGCCA AGTGTGGCT GACGCCAACCC	1200
CCACTGGTTG GGGCTTGGCC ATTGGCCATC AGCGCATGCG TGGAACCTTT GTGGCTCCTC	1260
TGCCGATCCA TACTGCGGAA CTCCCTGAG CTTGCTTCGC TCGCAGCCGG TCTGGAGCAA	1320
TCCTCATCGG CACAGACAAT TCTGTCGTCC TCTCCCGAA GTATACATCC TTTCCATGGC	1380
TGCTCGGATG TGCTGCCAAC TGGATCCTGC GCGGGACGTC CTTTGTGTTAC GTCCCGTCGG	1440
CGCTGAATCC AGCGGACGAA CCCTCCCGGG GCCGCTTGGG GCTCTACCGC CCTCTTCTGC	1500
GCTGCCGTT CCAGCCGACC ACGGGTCGCA CCTCTCTTTA CGCGGACTCC CCGTCTGTC	1560
CTTCTCATCT GCCGGTCCGT GTGCACCTCG CTTCACCTCT GCACGTCGCA TGGAGACAC	1620

CGTGAACGCC CCCTGGAGTT TGCCAACAGT CTTACATAAG AGGACTATTG GACTTCAGG	1680
ACGGTCAATG ACCTGGATCG AAGAATACAT CAAAGACTGT GTATTTAAAG ACTGGGAGGA	1740
GCTGGGGAG GAGATCAGGT TAAAGGTCTT TGTACTAGGA GGCTGTAGGC ATAAATTGGT	1800
CTGCGCACCA GCACCATGCA ACTTTTCAC CTCTGCCAA TCATCTCTTG TTTATGTCCC	1860
ACTGTTCAAG CCTCCAAGCT GTGCCTTGGG TGGCTTGGG GCATGGACAT TGACCCTAT	1920
AAAGAATTG GAGCTCTGT GGAATTGTTG TCTTTTTGC CTTCTGACTT CTTTCCGTCA	1980
ATCCGAGACC TTCTCGACAC CGCCTCAGCT CTGTATCGGG ATGCGTTAGA GTCACCGGAA	2040
CATTGCACCC CCAATCATAAC CGCTCTCAGG CAAGCTATTT TGTGTTGGGG TGAATTAAATG	2100
ACTTTGGCTT CCTGGGTGGG CAATAATTG GAGGACCTG CAGCCAGGGA TTTAGTAGTT	2160
AACTATGTTA ACACAAATAT GGGCTTAAAG ATTAGACAAC TATTGTGGTT TCACATTCC	2220
TGCCTTACTT TTGGAAGAGA AACAGTTCTT GAGTATTGG TGCCCTTGG AGTGTGGATT	2280
CGCACTCCTC CAGCTTATAG ACCACCAAAT GCCCCATCC TATCCACACT TCCGGAAACT	2340
ACTGTTGTTA GACGACGAGG CAGGTCCCT AGAAGAAGAA CTCCCTCGCC TCGCAGACGA	2400
AGGTCTCAAT CGCCGCGTCG CAGAAGATCT CAATCTCCAG CTTCCCAATG TTAGTATTCC	2460
TTGGACTCAT AAGGTGGAA ATTTTACGGG GCTCTACTCT TCTACTGTAC CTGCTTCAA	2520
TCCTCACTGG TTAACTCCTT CTTTCCTGA TATTCAATTG CATCAAGACC TGATATCTAA	2580
ATGTGAACAA TTTGTAGGCC CACTTACCAA AAATGAATTG AGAAGGTTGA AATTGATTAT	2640
GCCAGCCAGA TTCTTCCTA AACTTACTAA ATATTCCCT CTGGAGAAAG ACATTAACC	2700
TTATTATCCA GAGCATGCAG TTAATCATTA TTTCAAAACC AGACATTATT TGCATACTTT	2760
ATGGAAGGCG GGAATTATATA ATAAGAGAGA ATCCACACGT AGCGCCTCAT TTTGTGGGTC	2820
ACCATATTCT TGGGAACAAG AGCTACAGCA TGGGAGCACC TCTCTCAACG ACAAGAAGGG	2880
GCATGGGACA GAATCTCTCT GTGCCCAATC CACTGGGATT CTTCCAGAC CATCAACTGG	2940
ATCCTCTTTT CAGAGCAAAT TCCAGCAGTC CCGATTGGGA CTTCAACAAA AACAGGACA	3000
CTTGGCCAAT GGAAACAAG GTAGGAGTGG GAGGTTACGG TCCAGGGTTC ACACCCCCAC	-3060
ACGGTGGCCT GTGGGGTGG AGCCCTCAGG CACAAGGTGT TCTAACAAACC TTGCCAGCAG	3120
ATCCGCCTCC TGCCTCCACC AATCGGCTGT CCGGGAGGAA GCCAACCCCA GTCTCTCCAC	3180
CTCTAAGAGA CACACATCCA CAGGCAATGC AGTGG	3215

(2) INFORMATION FOR SEQ ID NO: 313:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3215 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 313:

AACTCAACCC	AGTTCCACCA	AGCTCTGTTG	GATCCCAGGG	TAAGGGCTCT	GTACTTCCCT	60
GCTGGTGGCT	CCAGTTCAAGG	GACACAGAAC	CCTGCTCCGA	CTATTGCCTC	TCTCACATCA	120
TCAATCTTCT	CGAAGACTGG	GGGCCCTGCT	ATGAACATGG	ACAACATTAC	ATCAGGACTC	180
CTAGGACCCC	TGCTCGTGTT	ACAGGCGGTG	TGTTTCTTGT	TGACAAAAAT	CCTCACAATA	240
CCACAGAGTC	TAGACTCGTG	GTGGACTTCT	CTCAATTTC	TAGGGGGACT	ACCCGGGTGT	300
CCTGGCCAAA	ATT CGCAGTC	CCCAACCTCC	AATCACTTAC	CAACCTCCTG	TCCTCCA ACT	360
TGTCCTGGCT	ATCGTTGGAT	GTGTCTGCGG	CGTTTTATCA	TCTTCCTCTT	CATCCTGCTG	420
CTATGCCTCA	TCTTCTTGTT	GGTTCTTCTG	GA CTATCAAG	GTATGTTGCC	CGTTTGT C CT	480
CTACTTCCAG	GATCCACGAC	CACCAGCACG	GGACCC TGCA	AAACCTGCAC	AACTCTGCA	540
CAAGGAACCT	CTATGTTCC	CTCCTGTTGC	TGTTCCAAAC	CCTCGGACGG	AAACTGCACT	600
TGTATTCCCA	TCCC ATCATC	CTGGGCTTTA	GGAAAATACC	TATGGGAGTG	GGCCTCAGCC	660
CGTTTCTCCT	GGCTCAGTTT	ACTAGTGCAA	TTTGTTCAGT	GGTGC GTC GG	GCTTTCCCCC	720
ACTGTTGGC	TTTTAGTTAT	ATGGATGATC	TGGTATTGGG	GGCCAAATCT	GTGCAGGATC	780
TTGAGTCCCT	TTATACCGCT	GTTACCAATT	TTCTGTTATC	TGTGGGTATC	CATTTAAATA	840
CCTCTAAAAC	AAAAAGATGG	GGTTACTCCC	TACATTTAT	GGGTTATGTC	ATTGGTAGTT	900
GGGGATCATT	ACCCCAAGAT	CACATTGTAC	ACAAAATCAA	GGAATGCTTT	CGAAA ACTGC	960
CTGTAAATCG	TCCAATTGAT	TGGAAAGTTT	GTCAACGCAT	AGTGGGTCTT	TTGGGCTTTG	1020
CTGCCCTTT	CACCC AATGC	GGTTATCCTG	CTCTCATGCC	TCTGTATGCC	TGTATTACTG	1080
CTAACACAGGC	TTTTGTCTTC	TCGCCAACCT	ACAAGGCCTT	TCTGTGTAAA	CAATACATGA	1140
ACCTTTACCC	GGTTGCTCGG	CAACGGCCAG	GCCTGTGCCA	AGTGTGTTGCT	GACGCCAACCC	1200
CCACTGGTTG	GGGCTTGGCC	ATTGGCCATC	AGCGCATGCG	TGGAACCTTT	GTGGCTCCTC	1260
TGCCGATCCA	TACTGCGGAA	CTCCTAGCAG	CTTGTGTTCGC	TCGCAGCAGG	TCTGGAGCGA	1320
CTCTCATCGG	CACGGACAAT	TCTGTTGTCC	TCTCTAGGAA	GTACACCTCC	TTTCCATGGC	1380
TGCTCGGATG	TGCTGCAAAC	TGGATCCTGC	GC GGGACGTC	CTTTGTTTAC	GTCCCATCGG	1440
CGCTGAATCC	CGCGGACGAC	CCCTCCC GGG	GCCGCTTGGG	GCTGTACCGC	CCTCTTCTCC	1500
GTCTGCCGTT	CCAGCCGACG	ACGGGTGCGA	CCTCTCTTTA	CGCGGACTCC	CCGTCTGTTC	1560
CTTCTCATCT	GCCGGACCGT	GTGCACTTCG	CTTCACCTCT	GCACGTGCA	TGGAGACCAC	1620
CGTGAACGCC	CCCTGGAGTT	TGCCAACAGT	CTTACATAAG	CGGACTCTTG	GACTTTCA GG	1680
ATGGTCAATG	ACCTGGATCG	AAGAATACAT	CAAAGACTGT	GTATTTAAGG	ACTGGGAGGA	1740
GTTGGGGAG	GAGATTAGGT	TAAAGGTCTT	TGTATTAGGA	GGCTGTAGGC	ATAAATTGGT	1800

CTGTTCACCA GCACCATGCA ACTTTTCAC CTCTGCCTAA TCATCTTTG TTCATGTCCC 1860  
ACTGTTCAAG CCTCCAAGCT GTGCCCTGGG TGGCTTGGA GCATGGACAT TGACCCATTAT 1920  
AAAGAATTG GAGCTCTGT GGAGTTACTC TCGTTTTGC CTTCTGATTT CTTCCCATCG 1980  
GTTCGGGACC TACTCGACAC CGCTTCAGCT CTTTACCGGG ATGCTTTAGA GTCACCTGAA 2040  
CATTGCACTC CCAACCATAAC TGCTCTCAGG CAAGCTATTT TGTGTTGGGG TGAGTTAAC 2100  
ACTTTGGCTT CCTGGGTGGG CAATAATTG GAGGACCCCTG CAGCTAGGGA TTTAGTAGTT 2160  
AACTATGTTA ACACTAACAT GGGCCTAAAA ATTAGACAAC TGTGTTGGGT TCACATTTCC 2220  
TGCCTTACTT TTGGAAGAGA AACAGTTCTA GAGTATTG TGTCTTTGG AGTGTGGATT 2280  
CGCACTCCTC CTGCTTACAG ACCACCAAAT GCCCCTATCC TATCCACACT TCCGGAAACT 2340  
ACTGTTGTTA GACGACGAGG CAGGTCCCC AGAAGAAGAA CTCCCTCGCC TCGCAGACGA 2400  
AGATCTCAAT CGCCGCGTCG CCGCAGATCT CAATCTCCAG CTTCCCAATG TTAGTATTCC 2460  
TTGGACTCAT AAGGTGGAA ACTTTACGGG GCTTACTCT TCTACTGTGC CTGCTTTAA 2520  
TCCTAACTGG TCCACTCCTT CTTTCTGA TATTCAATTG CATCAAGACC TGATTCTAA 2580  
ATGTGAACAA TTTGTAGGCC CACTTACTAA AAATGAATTAA CGAAGATTAA AATTGGTTAT 2640  
GCCAGCTAGA TTTTATCCTA AGGTTACCAA ATATTTCCC ATGGATAAAAG GCATCAAACC 2700  
CTATTATCCT GAGCATGCAG TTAATCATTAA CTTAAAAACC AGACATTATT TGCATACTTT 2760  
ATGGAAGGCG GGAATTTAT ATAAGAGAGA ATCCACACGT AGCGCCTCAT TTTGTGGGTC 2820  
ACCATATTCC TGGGAACAAG AGCTACAGCA TGGGAGCACC TCTCTCAACG ACACGAAGAG 2880  
GCATGGGACA GAATCTCTCT GTGCCCAATC CTCTGGGATT CTTCCAGAC CATCAGCTGG 2940  
ATCCGCTATT CAGAGCAAAT TCCAGCAGTC CCGACTGGGA CTTCAACACA AACAAAGGACA 3000  
GTTGGCCAAT GGCAAACAAG GTAGGAGTGG GAGGCTACGG TCCAGGGTTC ACACCCCCAC 3060  
ACGGTGGCCT GCTGGGTGG AGCCCTCAAG CACAAGGTGT GTTAACAACC TTGCCAGCAG 3120  
ATCCGCCTCC TGCTTCCACC AATCGGCGGT CCGGGAGAAA GCCAACCCCA GTCTCTCCAC 3180  
CTCTAAGAGA CACACATCCA CAGGCAATGC AGTGG 3215